GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: August 16, 2007, 22:48:51 ; Search time 73 Seconds
(without alignments)
43.032 Million cell updates/sec

Title: US-10-715-895A-4
Perfect score: 105
Sequence: 1 PVLDLFRELLNELLEALKQKLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 983262 seqs, 142787483 residues

Total number of hits satisfying chosen parameters: 983262

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS2/ptodata/1/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS2/ptodata/1/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS2/ptodata/1/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS2/ptodata/1/iaa/H_COMB.pep:*
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6: /EMC_Celerra_SIDS2/ptodata/1/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS2/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	105	100.0	22	2	US-08-940-095-4	Sequence 4, Appli
2	105	100.0	22	2	US-08-940-095-30	Sequence 30, Appl
3	105	100.0	22	2	US-08-940-095-100	Sequence 100, App
4	105	100.0	22	2	US-08-940-093-4	Sequence 4, Appli
5	105	100.0	22	2	US-08-940-093-30	Sequence 30, Appl
6	105	100.0	22	2	US-08-940-093-100	Sequence 100, App
7	105	100.0	22	2	US-08-940-096-4	Sequence 4, Appli
8	105	100.0	22	2	US-08-940-096-30	Sequence 30, Appl
9	105	100.0	22	2	US-08-940-096-100	Sequence 100, App
10	105	100.0	22	2	US-09-465-719-4	Sequence 4, Appli
11	105	100.0	22	2	US-09-465-719-30	Sequence 30, Appl
12	105	100.0	22	2	US-09-465-719-100	Sequence 100, App
13	105	100.0	22	2	US-08-942-597-1	Sequence 1, Appli
14	105	100.0	22	2	US-09-453-605-4	Sequence 4, Appli
15	105	100.0	22	2	US-09-453-605-30	Sequence 30, Appl
16	105	100.0	22	2	US-09-453-605-100	Sequence 100, App
17	105	100.0	22	2	US-09-453-838-4	Sequence 4, Appli
18	105	100.0	22	2	US-09-453-838-30	Sequence 30, Appl
19	105	100.0	22	2	US-09-453-838-100	Sequence 100, App
20	105	100.0	22	2	US-08-940-136-4	Sequence 4, Appli
21	105	100.0	22	2	US-08-940-136-30	Sequence 30, Appl
22	105	100.0	22	2	US-08-940-136-100	Sequence 100, App
23	105	100.0	22	2	US-09-453-841-4	Sequence 4, Appli
* 24	105	100.0	22	2	US-09-453-841-30	Sequence 30, Appl
25	105	100.0	22	2	US-09-453-841-100	Sequence 100, App
26	105	100.0	22	2	US-09-453-833-4	Sequence 4, Appli
27	105	100.0	22	2	US-09-453-833-30	Sequence 30, Appl
28	105	100.0	22	2	US-09-453-833-100	Sequence 100, App
29	105	100.0	22	2	US-09-453-826-4	Sequence 4, Appli
30	105	100.0	22	2	US-09-453-826-30	Sequence 30, Appl
31	105	100.0	22	2	US-09-453-826-100	Sequence 100, App
32	105	100.0	22	2	US-09-453-840-4	Sequence 4, Appli
33	105	100.0	22	2	US-09-453-840-30	Sequence 30, Appl
34	105	100.0	22	2	US-09-453-840-100	Sequence 100, App
35	105	100.0	22	2	US-09-865-989-4	Sequence 4, Appli
36	105	100.0	22	2	US-09-865-989-30	Sequence 30, Appl
37	105	100.0	22	2	US-09-865-989-100	Sequence 100, App
38	105	100.0	22	2	US-09-453-834-4	Sequence 4, Appli
39	105	100.0	22	2	US-09-453-834-30	Sequence 30, Appl
40	105	100.0	22	2	US-09-453-834-100	Sequence 100, App
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42	105	100.0	22	2	US-10-283-599-30	Sequence 30, Appl
43	105	100.0	22	2	US-10-283-599-100	Sequence 100, App
44	105	100.0	22	2	US-09-465-718-4	Sequence 4, Appli
45	105	100.0	22	2	US-09-465-718-30	Sequence 30, Appl

ALIGNMENTS

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RESULT 1
US-08-940-095-4
; Sequence 4, Application US/08940095
; Patent No. 6004925
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    APPLICANT:  Dufourcq, Jean
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,095
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0004-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6004925e
US-08-940-095-4
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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
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Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 2
US-08-940-095-30
; Sequence 30, Application US/08940095
; Patent No. 6004925
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    APPLICANT:  Dufourcq, Jean
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,095
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0004-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6004925e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  N-terminal dansylated peptide
US-08-940-095-30

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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 3
US-08-940-095-100
; Sequence 100, Application US/08940095
; Patent No. 6004925
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    APPLICANT:  Dufourcq, Jean
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,095
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0004-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6004925e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  All amino acids are in the D-configuration
US-08-940-095-100

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 4
US-08-940-093-4
; Sequence 4, Application US/08940093
; Patent No. 6037323
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
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;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,093
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0006-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6037323e
US-08-940-093-4

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 5
US-08-940-093-30
; Sequence 30, Application US/08940093
; Patent No. 6037323
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,093
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0006-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6037323e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  N-terminal dansylated peptide
US-08-940-093-30

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Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 6
US-08-940-093-100
; Sequence 100, Application US/08940093
; Patent No. 6037323
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,093
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0006-999
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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6037323e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  All amino acids are in the D-configuration
US-08-940-093-100

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 7
US-08-940-096-4
; Sequence 4, Application US/08940096
; Patent No. 6046166
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,096
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0005-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6046166e
US-08-940-096-4

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
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Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 8
US-08-940-096-30
; Sequence 30, Application US/08940096
; Patent No. 6046166
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
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;      APPLICATION NUMBER:  US/08/940,096
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0005-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6046166e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  N-terminal dansylated peptide
US-08-940-096-30

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
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Db          1 PVLDLFRELLNELLEALKQKLK 22
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RESULT 9
US-08-940-096-100
; Sequence 100, Application US/08940096
; Patent No. 6046166
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,096
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0005-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6046166e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  All amino acids are in the D-configuration
US-08-940-096-100

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  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 10
US-09-465-719-4
; Sequence 4, Application US/09465719
; Patent No. 6265377
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/465,719
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/940,093
;      FILING DATE:  29-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0006-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6265377e
US-09-465-719-4

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 11
US-09-465-719-30
; Sequence 30, Application US/09465719
; Patent No. 6265377
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/09/465,719
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/940,093
;      FILING DATE:  29-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0006-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6265377e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  N-terminal dansylated peptide
US-09-465-719-30

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 12
US-09-465-719-100
; Sequence 100, Application US/09465719
; Patent No. 6265377
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/465,719
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/940,093
;      FILING DATE:  29-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0006-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6265377e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  All amino acids are in the D-configuration
US-09-465-719-100

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 13
US-08-942-597-1
; Sequence 1, Application US/08942597
; Patent No. 6287590
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    TITLE OF INVENTION:  PEPTIDE/LIPID COMPLEX FORMATION
;    TITLE OF INVENTION:  BY CO-LYOPHILIZATION
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds, LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/942,597
;      FILING DATE:  02-OCT-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  9196-0008-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-942-597-1

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 PVLDLFRELLNELLEALKQKLK 22
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Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 14
US-09-453-605-4
; Sequence 4, Application US/09453605
; Patent No. 6329341
;   GENERAL INFORMATION:
;        APPLICANT: Dasseux, Jean-Louis
;                   Sekul, Renate
;                   Buttner, Klaus
;                   Cornut, Isabelle
;                   Metz, Gunther
;                   Dufourcq, Jean
;        TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                            AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;        NUMBER OF SEQUENCES: 258
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/453,605
;             FILING DATE: 26-No. 6329341-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/940,095
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Coruzzi, Laura A
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 009196-0004-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 22 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: No. 6329341e
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-453-605-4

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 15
US-09-453-605-30
; Sequence 30, Application US/09453605
; Patent No. 6329341
;   GENERAL INFORMATION:
;        APPLICANT: Dasseux, Jean-Louis
;                   Sekul, Renate
;                   Buttner, Klaus
;                   Cornut, Isabelle
;                   Metz, Gunther
;                   Dufourcq, Jean
;        TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                            AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;        NUMBER OF SEQUENCES: 258
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/453,605
;             FILING DATE: 26-No. 6329341-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/940,095
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Coruzzi, Laura A
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 009196-0004-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 30:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 22 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: No. 6329341e
;        FEATURE:
;             NAME/KEY:  Other
;             LOCATION:  1...22
;             OTHER INFORMATION:  N-terminal dansylated peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-453-605-30

  Query Match             100.0%;  Score 105;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


Search completed: August 16, 2007, 22:50:33
Job time : 74 secs
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GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: August 16, 2007, 22:49:31 ; Search time 300 Seconds
(without alignments)
59.976 Million cell updates/sec

Title: US-10-715-895A-4
Perfect score: 105
Sequence: 1 PVLDLFRELLNELLEALKQKLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3552611 seqs, 817857308 residues

Total number of hits satisfying chosen parameters: 3552611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	105	100.0	22	3	US-09-865-989-4	Sequence 4, Appli
2	105	100.0	22	3	US-09-865-989-30	Sequence 30, Appl
3	105	100.0	22	3	US-09-865-989-100	Sequence 100, App
4	105	100.0	22	3	US-09-865-989-4	Sequence 4, Appli
5	105	100.0	22	3	US-09-865-989-30	Sequence 30, Appl
6	105	100.0	22	3	US-09-865-989-100	Sequence 100, App
7	105	100.0	22	4	US-10-099-574A-4	Sequence 4, Appli
8	105	100.0	22	4	US-10-099-574A-30	Sequence 30, Appl
9	105	100.0	22	4	US-10-099-574A-100	Sequence 100, App
10	105	100.0	22	4	US-10-252-940-1	Sequence 1, Appli
11	105	100.0	22	4	US-10-099-836B-4	Sequence 4, Appli
12	105	100.0	22	4	US-10-099-836B-30	Sequence 30, Appl
13	105	100.0	22	4	US-10-099-836B-100	Sequence 100, App
14	105	100.0	22	4	US-10-283-599-4	Sequence 4, Appli
15	105	100.0	22	4	US-10-283-599-30	Sequence 30, Appl
16	105	100.0	22	4	US-10-283-599-100	Sequence 100, App
17	105	100.0	22	4	US-10-802-080-4	Sequence 4, Appli
18	105	100.0	22	4	US-10-802-080-30	Sequence 30, Appl
19	105	100.0	22	4	US-10-802-080-100	Sequence 100, App
20	105	100.0	22	4	US-10-801-897-4	Sequence 4, Appli
21	105	100.0	22	4	US-10-801-897-30	Sequence 30, Appl
22	105	100.0	22	4	US-10-801-897-100	Sequence 100, App
23	105	100.0	22	5	US-10-937-767-4	Sequence 4, Appli
24	105	100.0	22	5	US-10-937-767-30	Sequence 30, Appl
25	105	100.0	22	5	US-10-937-767-100	Sequence 100, App
26	105	100.0	22	5	US-10-991-217-4	Sequence 4, Appli
27	105	100.0	22	5	US-10-991-217-30	Sequence 30, Appl
28	105	100.0	22	5	US-10-991-217-100	Sequence 100, App
29	105	100.0	22	5	US-10-099-574A-4	Sequence 4, Appli
30	105	100.0	22	5	US-10-099-574A-30	Sequence 30, Appl
31	105	100.0	22	5	US-10-099-574A-100	Sequence 100, App
32	105	100.0	22	5	US-10-715-895-4	Sequence 4, Appli
33	105	100.0	22	5	US-10-715-895-30	Sequence 30, Appl
34	105	100.0	22	5	US-10-715-895-100	Sequence 100, App
35	105	100.0	22	6	US-11-482-292-4	Sequence 4, Appli
36	105	100.0	22	6	US-11-482-292-30	Sequence 30, Appl
37	105	100.0	22	6	US-11-482-292-100	Sequence 100, App
38	105	100.0	22	6	US-11-683-784-1	Sequence 1, Appli
39	102	97.1	22	3	US-09-865-989-7	Sequence 7, Appli
40	102	97.1	22	3	US-09-865-989-7	Sequence 7, Appli
41	102	97.1	22	4	US-10-099-574A-7	Sequence 7, Appli
42	102	97.1	22	4	US-10-099-836B-7	Sequence 7, Appli
43	102	97.1	22	4	US-10-283-599-7	Sequence 7, Appli
44	102	97.1	22	4	US-10-802-080-7	Sequence 7, Appli
45	102	97.1	22	4	US-10-801-897-7	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
US-09-865-989-4
; Sequence 4, Application US/09865989
; Publication No. US20030008827A1
;   GENERAL INFORMATION:
;        APPLICANT: Dasseux, Jean-Louis
;                   Sekul, Renate
;                   Buttner, Klaus
;                   Cornut, Isabelle
;                   Metz, Gunther
;        TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                            AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;        NUMBER OF SEQUENCES: 258
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/865,989
;             FILING DATE: 25-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/465,719
;             FILING DATE: 17-DEC-1999
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Coruzzi, Laura A
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 009196-0006-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 22 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: No. US20030008827A1e
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-865-989-4
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  Query Match             100.0%;  Score 105;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 2
US-09-865-989-30
; Sequence 30, Application US/09865989
; Publication No. US20030008827A1
;   GENERAL INFORMATION:
;        APPLICANT: Dasseux, Jean-Louis
;                   Sekul, Renate
;                   Buttner, Klaus
;                   Cornut, Isabelle
;                   Metz, Gunther
;        TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                            AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;        NUMBER OF SEQUENCES: 258
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/865,989
;             FILING DATE: 25-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/465,719
;             FILING DATE: 17-DEC-1999
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Coruzzi, Laura A
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 009196-0006-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 30:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 22 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: No. US20030008827A1e
;        FEATURE:
;             NAME/KEY:  Other
;             LOCATION:  1...22
;             OTHER INFORMATION:  N-terminal dansylated peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-865-989-30

  Query Match             100.0%;  Score 105;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 3
```

```
US-09-865-989-100
; Sequence 100, Application US/09865989
; Publication No. US20030008827A1
;   GENERAL INFORMATION:
;        APPLICANT: Dasseux, Jean-Louis
;                   Sekul, Renate
;                   Buttner, Klaus
;                   Cornut, Isabelle
;                   Metz, Gunther
;        TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                            AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;        NUMBER OF SEQUENCES: 258
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/865,989
;             FILING DATE: 25-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/465,719
;             FILING DATE: 17-DEC-1999
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Coruzzi, Laura A
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 009196-0006-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 100:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 22 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: No. US20030008827A1e
;        FEATURE:
;             NAME/KEY:  Other
;             LOCATION:  1...22
;             OTHER INFORMATION:  All amino acids are in the D-configuration
;        SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-865-989-100

  Query Match             100.0%;  Score 105;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 4
US-09-865-989-4
; Sequence 4, Application US/09865989
; Publication No. US20040029807A9
;   GENERAL INFORMATION:
;        APPLICANT: Dasseux, Jean-Louis
;                   Sekul, Renate
;                   Buttner, Klaus
;                   Cornut, Isabelle
;                   Metz, Gunther
;        TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
```

```
;                          AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;       NUMBER OF SEQUENCES: 258
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036-2811
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/865,989
;            FILING DATE: 25-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/465,719
;            FILING DATE: 17-DEC-1999
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Coruzzi, Laura A
;            REGISTRATION NUMBER: 30,742
;            REFERENCE/DOCKET NUMBER: 009196-0006-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-493-4935
;            TELEFAX: 650-493-5556
;            TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 22 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: No. US20040029807A9e
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-865-989-4

  Query Match           100.0%;  Score 105;  DB 3;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 5
US-09-865-989-30
; Sequence 30, Application US/09865989
; Publication No. US20040029807A9
;   GENERAL INFORMATION:
;       APPLICANT: Dasseux, Jean-Louis
;                  Sekul, Renate
;                  Buttner, Klaus
;                  Cornut, Isabelle
;                  Metz, Gunther
;       TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                           AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;       NUMBER OF SEQUENCES: 258
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036-2811
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/865,989
;            FILING DATE: 25-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/465,719
;            FILING DATE: 17-DEC-1999
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Coruzzi, Laura A
;            REGISTRATION NUMBER: 30,742
;            REFERENCE/DOCKET NUMBER: 009196-0006-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-493-4935
;            TELEFAX: 650-493-5556
;            TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 30:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 22 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: No. US20040029807A9e
;       FEATURE:
;            NAME/KEY:  Other
;            LOCATION:  1...22
;            OTHER INFORMATION:  N-terminal dansylated peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-865-989-30

  Query Match           100.0%;  Score 105;  DB 3;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 6
US-09-865-989-100
; Sequence 100, Application US/09865989
; Publication No. US20040029807A9
;   GENERAL INFORMATION:
;       APPLICANT: Dasseux, Jean-Louis
;                  Sekul, Renate
;                  Buttner, Klaus
;                  Cornut, Isabelle
;                  Metz, Gunther
;       TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                           AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;       NUMBER OF SEQUENCES: 258
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036-2811
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/865,989
;            FILING DATE: 25-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/465,719
;            FILING DATE: 17-DEC-1999
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Coruzzi, Laura A
;            REGISTRATION NUMBER: 30,742
```

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;            REFERENCE/DOCKET NUMBER: 009196-0006-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-493-4935
;            TELEFAX: 650-493-5556
;            TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 100:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 22 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: No. US20040029807A9e
;       FEATURE:
;            NAME/KEY:  Other
;            LOCATION:  1...22
;            OTHER INFORMATION:  All amino acids are in the D-configuration
;       SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-865-989-100

  Query Match             100.0%;  Score 105;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 7
US-10-099-574A-4
; Sequence 4, Application US/10099574A
; Publication No. US20030060604A1
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  254
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/099,574A
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0005-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. US20030060604A1e
US-10-099-574A-4

  Query Match             100.0%;  Score 105;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 8
US-10-099-574A-30
; Sequence 30, Application US/10099574A
; Publication No. US20030060604A1
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  254
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/099,574A
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0005-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. US20030060604A1e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  N-terminal dansylated peptide
US-10-099-574A-30

  Query Match             100.0%;  Score 105;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22
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```
RESULT 9
US-10-099-574A-100
; Sequence 100, Application US/10099574A
; Publication No. US20030060604A1
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  254
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/099,574A
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0005-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. US20030060604A1e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  All amino acids are in the D-configuration
US-10-099-574A-100

  Query Match             100.0%;  Score 105;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 10
US-10-252-940-1
; Sequence 1, Application US/10252940
; Publication No. US20030099714A1
;  GENERAL INFORMATION:
;       APPLICANT: Dasseux, Jean-Louis
;       TITLE OF INVENTION: PEPTIDE/LIPID COMPLEX FORMATION
;                           BY CO-LYOPHILIZATION
;       NUMBER OF SEQUENCES: 1
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds, LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036-2811
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows
;            SOFTWARE: FastSEQ for Windows Version 2.0b
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/252,940
;            FILING DATE: 23-Sep-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/942,597
;            FILING DATE: 02-OCT-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Coruzzi, Laura A
;            REGISTRATION NUMBER: 30,742
;            REFERENCE/DOCKET NUMBER: 9196-0008-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-493-4935
;            TELEFAX: 650-493-5556
;            TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 22 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-252-940-1

  Query Match             100.0%;  Score 105;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 11
US-10-099-836B-4
; Sequence 4, Application US/10099836B
; Publication No. US20030203842A1
;  GENERAL INFORMATION:
;       APPLICANT: Dasseux, Jean-Louis
;                  Sekul, Renate
;                  Buttner, Klaus
;                  Cornut, Isabelle
;                  Metz, Gunther
;                  Dufourcq, Jean
;       TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                           AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;       NUMBER OF SEQUENCES: 254
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036-2811
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/099,836B
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;             FILING DATE: 28-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Coruzzi, Laura A
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 009196-0004-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 22 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: No. US20030203842A1e
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-099-836B-4

  Query Match             100.0%;  Score 105;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 12
US-10-099-836B-30
; Sequence 30, Application US/10099836B
; Publication No. US20030203842A1
;   GENERAL INFORMATION:
;        APPLICANT: Dasseux, Jean-Louis
;                   Sekul, Renate
;                   Buttner, Klaus
;                   Cornut, Isabelle
;                   Metz, Gunther
;                   Dufourcq, Jean
;        TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                            AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;        NUMBER OF SEQUENCES: 254
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/099,836B
;             FILING DATE: 28-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Coruzzi, Laura A
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 009196-0004-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 30:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 22 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: No. US20030203842A1e
;        FEATURE:
;             NAME/KEY:  Other
;             LOCATION:  1...22
;             OTHER INFORMATION:  N-terminal dansylated peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-099-836B-30

  Query Match             100.0%;  Score 105;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 13
US-10-099-836B-100
; Sequence 100, Application US/10099836B
; Publication No. US20030203842A1
;   GENERAL INFORMATION:
;        APPLICANT: Dasseux, Jean-Louis
;                   Sekul, Renate
;                   Buttner, Klaus
;                   Cornut, Isabelle
;                   Metz, Gunther
;                   Dufourcq, Jean
;        TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;                            AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;        NUMBER OF SEQUENCES: 254
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/099,836B
;             FILING DATE: 28-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Coruzzi, Laura A
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 009196-0004-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 100:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 22 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: No. US20030203842A1e
;        FEATURE:
;             NAME/KEY:  Other
```

```
;             LOCATION:  1...22
;             OTHER INFORMATION:  All amino acids are in the D-configuration
;        SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-099-836B-100

  Query Match           100.0%;  Score 105;  DB 4;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 14
US-10-283-599-4
; Sequence 4, Application US/10283599
; Publication No. US20030208059A1
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    APPLICANT:  Dufourcq, Jean
;    TITLE OF INVENTION:  GENE THERAPY APPROACHES TO
;    TITLE OF INVENTION:  SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
;    TITLE OF INVENTION:  USE TO TREAT DYSLIPIDEMIC DISORDERS.
;    NUMBER OF SEQUENCES:  274
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/283,599
;      FILING DATE:  29-OCT-2002
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/940,136
;      FILING DATE:  29-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0007-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. US20030208059A1e
US-10-283-599-4

  Query Match           100.0%;  Score 105;  DB 4;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


RESULT 15
US-10-283-599-30
; Sequence 30, Application US/10283599
; Publication No. US20030208059A1
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    APPLICANT:  Dufourcq, Jean
;    TITLE OF INVENTION:  GENE THERAPY APPROACHES TO
;    TITLE OF INVENTION:  SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
;    TITLE OF INVENTION:  USE TO TREAT DYSLIPIDEMIC DISORDERS.
;    NUMBER OF SEQUENCES:  274
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/283,599
;      FILING DATE:  29-OCT-2002
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/940,136
;      FILING DATE:  29-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0007-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. US20030208059A1e
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...22
;      OTHER INFORMATION:  N-terminal dansylated peptide
US-10-283-599-30

  Query Match           100.0%;  Score 105;  DB 4;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-07;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              ||||||||||||||||||||||
Db          1 PVLDLFRELLNELLEALKQKLK 22


Search completed: August 16, 2007, 22:55:39
Job time : 301 secs
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: August 16, 2007, 22:50:51 ; Search time 7 Seconds
(without alignments)
3.121 Million cell updates/sec

Title: US-10-715-895A-4
Perfect score: 105
Sequence: 1 PVLDLFRELLNELLEALKQKLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5387 seqs, 993155 residues

Total number of hits satisfying chosen parameters: 5387

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS2/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	39.0	900	1	US-10-533-069-1050	Sequence 1050, Ap
2	39	37.1	2000	1	US-10-533-069-452	Sequence 452, App
3	38	36.2	154	1	US-10-533-069-1216	Sequence 1216, Ap
4	38	36.2	232	1	US-10-533-069-2353	Sequence 2353, Ap
5	38	36.2	1154	1	US-10-533-069-1039	Sequence 1039, Ap
6	37.5	35.7	1132	1	US-10-533-069-1070	Sequence 1070, Ap
7	37	35.2	508	1	US-10-533-069-432	Sequence 432, App
8	37	35.2	1427	1	US-10-533-069-1043	Sequence 1043, Ap
9	36	34.3	461	1	US-10-533-069-1242	Sequence 1242, Ap
10	36	34.3	491	1	US-10-533-069-1156	Sequence 1156, Ap
11	36	34.3	491	1	US-10-533-069-1158	Sequence 1158, Ap
12	36	34.3	997	1	US-10-533-069-565	Sequence 565, App
13	35.5	33.8	1220	1	US-10-533-069-141	Sequence 141, App
14	35.5	33.8	1359	7	US-11-657-313-3	Sequence 3, Appli
15	35.5	33.8	2030	7	US-11-657-313-24	Sequence 24, Appl
16	35	33.3	553	7	US-11-725-235-116	Sequence 116, App
17	34.5	32.9	1333	7	US-11-657-313-23	Sequence 23, Appl
18	34	32.4	325	1	US-10-533-069-1316	Sequence 1316, Ap
19	34	32.4	544	1	US-10-533-069-121	Sequence 121, App
20	34	32.4	1097	1	US-10-533-069-943	Sequence 943, App
21	34	32.4	1440	1	US-10-533-069-100	Sequence 100, App
22	33.5	31.9	373	7	US-11-539-856-23	Sequence 23, Appl
23	33.5	31.9	373	7	US-11-539-856-31	Sequence 31, Appl
24	33.5	31.9	431	7	US-11-725-235-192	Sequence 192, App
25	33.5	31.9	467	7	US-11-725-235-170	Sequence 170, App
26	33.5	31.9	815	7	US-11-551-744-236	Sequence 236, App
27	33.5	31.9	1647	1	US-10-533-069-735	Sequence 735, App
28	33.5	31.9	2000	1	US-10-533-069-860	Sequence 860, App
29	33.5	31.9	2000	1	US-10-533-069-1015	Sequence 1015, Ap
30	33.5	31.9	2022	7	US-11-551-744-292	Sequence 292, App
31	33.5	31.9	3433	1	US-10-533-069-1600	Sequence 1600, Ap
32	33	31.4	333	1	US-10-533-069-725	Sequence 725, App
33	33	31.4	378	1	US-10-533-069-855	Sequence 855, App
34	33	31.4	511	1	US-10-533-069-1288	Sequence 1288, Ap
35	33	31.4	560	1	US-10-533-069-1172	Sequence 1172, Ap
36	33	31.4	608	1	US-10-523-312A-9	Sequence 9, Appli
37	33	31.4	608	1	US-10-523-312A-10	Sequence 10, Appl
38	33	31.4	808	1	US-10-533-069-1976	Sequence 1976, Ap
39	33	31.4	1960	7	US-11-656-389-74	Sequence 74, Appl
40	33	31.4	1961	7	US-11-656-389-15	Sequence 15, Appl
41	33	31.4	2505	7	US-11-656-389-3	Sequence 3, Appli
42	32.5	31.0	256	1	US-10-533-069-1182	Sequence 1182, Ap
43	32.5	31.0	342	7	US-11-711-935-1	Sequence 1, Appli
44	32.5	31.0	1396	1	US-10-533-069-707	Sequence 707, App
45	32.5	31.0	2000	1	US-10-533-069-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-533-069-1050
; Sequence 1050, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL,SUDEEPTA
; APPLICANT: CLARK,HILARY
; APPLICANT: GURNEY,AUSTIN L.
; APPLICANT: SCHOENFELD,JILL
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD,WILLIAM I.
; APPLICANT: WU,THOMAS D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1982R1 US
; CURRENT APPLICATION NUMBER: US/10/533,069
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/34381
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 60/422,472
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 1050
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-069-1050

Query Match 39.0%; Score 41; DB 1; Length 900;
Best Local Similarity 42.1%; Pred. No. 13;
Matches 8; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 VLDLFRELLNELLEALKQK 20
              |  ||::| |: :|:|:|:
Db        798 VSPLFQKLENDQIESLRQR 816
```

RESULT 2
US-10-533-069-452
; Sequence 452, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL,SUDEEPTA
; APPLICANT: CLARK,HILARY
; APPLICANT: GURNEY,AUSTIN L.
; APPLICANT: SCHOENFELD,JILL
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD,WILLIAM I.

; APPLICANT: WU,THOMAS D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1982R1 US
; CURRENT APPLICATION NUMBER: US/10/533,069
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/34381
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 60/422,472
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 452
; LENGTH: 2000
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-069-452

Query Match 37.1%; Score 39; DB 1; Length 2000;
Best Local Similarity 44.4%; Pred. No. 63;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

```
Qy          5 LFRELLNELLEALKQKLK 22
              :||||: ||   :|: |:
Db        997 VFRELVEELHPLMKEALE 1014
```

RESULT 3
US-10-533-069-1216
; Sequence 1216, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL,SUDEEPTA
; APPLICANT: CLARK,HILARY
; APPLICANT: GURNEY,AUSTIN L.
; APPLICANT: SCHOENFELD,JILL
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD,WILLIAM I.
; APPLICANT: WU,THOMAS D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1982R1 US
; CURRENT APPLICATION NUMBER: US/10/533,069
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/34381
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 60/422,472
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 1216
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-069-1216

Query Match 36.2%; Score 38; DB 1; Length 154;
Best Local Similarity 31.8%; Pred. No. 4.5;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 PVLDLFRELLNELLEALKQKLK 22
              | |:  :| : :::| | |:|:
Db         88 PALENNKEQIQKIIETLTQQLQ 109
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RESULT 4
US-10-533-069-2353
; Sequence 2353, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL,SUDEEPTA
; APPLICANT: CLARK,HILARY
; APPLICANT: GURNEY,AUSTIN L.
; APPLICANT: SCHOENFELD,JILL
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD,WILLIAM I.
; APPLICANT: WU,THOMAS D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1982R1 US
; CURRENT APPLICATION NUMBER: US/10/533,069
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/34381
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 60/422,472
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 2353
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-069-2353

Query Match 36.2%; Score 38; DB 1; Length 232;
Best Local Similarity 50.0%; Pred. No. 7.2;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```
Qy          8 ELLNELLEALKQKL 21
              |:|::|:|  |:||
Db        109 EMLDDLMEKRKEKL 122
```

RESULT 5
US-10-533-069-1039
; Sequence 1039, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL,SUDEEPTA
; APPLICANT: CLARK,HILARY
; APPLICANT: GURNEY,AUSTIN L.
; APPLICANT: SCHOENFELD,JILL
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD,WILLIAM I.
; APPLICANT: WU,THOMAS D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1982R1 US
; CURRENT APPLICATION NUMBER: US/10/533,069
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/34381
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US 60/422,472
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 1039
; LENGTH: 1154
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-069-1039

Query Match 36.2%; Score 38; DB 1; Length 1154;
Best Local Similarity 56.2%; Pred. No. 46;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

```
Qy          4 DLFRELLNELLEALKQ 19
              || :   || || |||
Db       1099 DLLKYAKNETLENLKQ 1114
```

RESULT 6
US-10-533-069-1070
; Sequence 1070, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL,SUDEEPTA
; APPLICANT: CLARK,HILARY
; APPLICANT: GURNEY,AUSTIN L.
; APPLICANT: SCHOENFELD,JILL

```
;  APPLICANT:  WILLIAMS, P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
;  TITLE OF INVENTION:  RELATED DISEASES
;  FILE REFERENCE: P1982R1 US
;  CURRENT APPLICATION NUMBER: US/10/533,069
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: PCT/US03/34381
;  PRIOR FILING DATE: 2003-10-28
;  PRIOR APPLICATION NUMBER: US 60/422,472
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 1070
;   LENGTH: 1132
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-533-069-1070

  Query Match             35.7%;  Score 37.5;  DB 1;  Length 1132;
  Best Local Similarity   39.4%;  Pred. No. 54;
  Matches   13;  Conservative    4;  Mismatches    3;  Indels   13;  Gaps    2;

Qy          2 VLDLFRELL----------NE-LLEALKQKL 21
              :|  |||||            || ||| |:|::
Db        612 LLQEFRELLQYRDNSDKTLEANEMLLEKLRQRI 644


RESULT 7
US-10-533-069-432
; Sequence 432, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
;  APPLICANT: AGGARWAL,SUDEEPTA
;  APPLICANT:  CLARK,HILARY
;  APPLICANT:  GURNEY,AUSTIN L.
;  APPLICANT:  SCHOENFELD,JILL
;  APPLICANT:  WILLIAMS, P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
;  TITLE OF INVENTION:  RELATED DISEASES
;  FILE REFERENCE: P1982R1 US
;  CURRENT APPLICATION NUMBER: US/10/533,069
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: PCT/US03/34381
;  PRIOR FILING DATE: 2003-10-28
;  PRIOR APPLICATION NUMBER: US 60/422,472
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 432
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-533-069-432

  Query Match             35.2%;  Score 37;  DB 1;  Length 508;
  Best Local Similarity   40.9%;  Pred. No. 25;
  Matches    9;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              | ||   ||  | || :  ::|
Db        149 PTLDKVLELQPEKLELIMDEMK 170


RESULT 8
US-10-533-069-1043
; Sequence 1043, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
;  APPLICANT: AGGARWAL,SUDEEPTA
;  APPLICANT:  CLARK,HILARY
;  APPLICANT:  GURNEY,AUSTIN L.
;  APPLICANT:  SCHOENFELD,JILL
;  APPLICANT:  WILLIAMS, P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
;  TITLE OF INVENTION:  RELATED DISEASES
;  FILE REFERENCE: P1982R1 US
;  CURRENT APPLICATION NUMBER: US/10/533,069
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: PCT/US03/34381
;  PRIOR FILING DATE: 2003-10-28
;  PRIOR APPLICATION NUMBER: US 60/422,472
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 1043
;   LENGTH: 1427
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-533-069-1043

  Query Match             35.2%;  Score 37;  DB 1;  Length 1427;
  Best Local Similarity   42.9%;  Pred. No. 83;
  Matches    9;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 VLDLFRELLNELLEALKQKLK 22
              | :| :||  || : |: |:|
Db       1381 VAELVKELRCELDQLLQDKIK 1401


RESULT 9
US-10-533-069-1242
; Sequence 1242, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
;  APPLICANT: AGGARWAL,SUDEEPTA
;  APPLICANT:  CLARK,HILARY
;  APPLICANT:  GURNEY,AUSTIN L.
;  APPLICANT:  SCHOENFELD,JILL
;  APPLICANT:  WILLIAMS, P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
;  TITLE OF INVENTION:  RELATED DISEASES
;  FILE REFERENCE: P1982R1 US
;  CURRENT APPLICATION NUMBER: US/10/533,069
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: PCT/US03/34381
;  PRIOR FILING DATE: 2003-10-28
;  PRIOR APPLICATION NUMBER: US 60/422,472
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 1242
;   LENGTH: 461
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-533-069-1242

  Query Match             34.3%;  Score 36;  DB 1;  Length 461;
  Best Local Similarity   50.0%;  Pred. No. 31;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 LFRELLNELLEALKQK 20
              | | :||| |: || :
Db        121 LMRMVLNESLKVLKMQ 136


RESULT 10
US-10-533-069-1156
; Sequence 1156, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
;  APPLICANT: AGGARWAL,SUDEEPTA
;  APPLICANT:  CLARK,HILARY
```

```
;  APPLICANT:  GURNEY,AUSTIN L.
;  APPLICANT:  SCHOENFELD,JILL
;  APPLICANT:  WILLIAMS, P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
;  TITLE OF INVENTION:  RELATED DISEASES
;  FILE REFERENCE: P1982R1 US
;  CURRENT APPLICATION NUMBER: US/10/533,069
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: PCT/US03/34381
;  PRIOR FILING DATE: 2003-10-28
;  PRIOR APPLICATION NUMBER: US 60/422,472
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 1156
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-533-069-1156

  Query Match             34.3%;  Score 36;  DB 1;  Length 491;
  Best Local Similarity   50.0%;  Pred. No. 34;
  Matches    6;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 LNELLEALKQKL 21
              | |::| :|||:
Db        361 LQEIVEGMKQKM 372


RESULT 11
US-10-533-069-1158
; Sequence 1158, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
;  APPLICANT: AGGARWAL,SUDEEPTA
;  APPLICANT:  CLARK,HILARY
;  APPLICANT:  GURNEY,AUSTIN L.
;  APPLICANT:  SCHOENFELD,JILL
;  APPLICANT:  WILLIAMS, P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
;  TITLE OF INVENTION:  RELATED DISEASES
;  FILE REFERENCE: P1982R1 US
;  CURRENT APPLICATION NUMBER: US/10/533,069
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: PCT/US03/34381
;  PRIOR FILING DATE: 2003-10-28
;  PRIOR APPLICATION NUMBER: US 60/422,472
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 1158
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-533-069-1158

  Query Match             34.3%;  Score 36;  DB 1;  Length 491;
  Best Local Similarity   50.0%;  Pred. No. 34;
  Matches    6;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 LNELLEALKQKL 21
              | |::| :|||:
Db        361 LQEIVEGMKQKM 372


RESULT 12
US-10-533-069-565
; Sequence 565, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
;  APPLICANT: AGGARWAL,SUDEEPTA
;  APPLICANT:  CLARK,HILARY
;  APPLICANT:  GURNEY,AUSTIN L.
;  APPLICANT:  SCHOENFELD,JILL
;  APPLICANT:  WILLIAMS, P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
;  TITLE OF INVENTION:  RELATED DISEASES
;  FILE REFERENCE: P1982R1 US
;  CURRENT APPLICATION NUMBER: US/10/533,069
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: PCT/US03/34381
;  PRIOR FILING DATE: 2003-10-28
;  PRIOR APPLICATION NUMBER: US 60/422,472
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 565
;   LENGTH: 997
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-533-069-565

  Query Match             34.3%;  Score 36;  DB 1;  Length 997;
  Best Local Similarity   43.8%;  Pred. No. 76;
  Matches    7;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          4 DLFRELLNELLEALKQ 19
              || :   || :| :||
Db        941 DLLKNAKNEAIENMKQ 956


RESULT 13
US-10-533-069-141
; Sequence 141, Application US/10533069
; Publication No. US20070185017A1
; GENERAL INFORMATION:
;  APPLICANT: AGGARWAL,SUDEEPTA
;  APPLICANT:  CLARK,HILARY
;  APPLICANT:  GURNEY,AUSTIN L.
;  APPLICANT:  SCHOENFELD,JILL
;  APPLICANT:  WILLIAMS, P. MICKEY
;  APPLICANT:  WOOD,WILLIAM I.
;  APPLICANT:  WU,THOMAS D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
;  TITLE OF INVENTION:  RELATED DISEASES
;  FILE REFERENCE: P1982R1 US
;  CURRENT APPLICATION NUMBER: US/10/533,069
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: PCT/US03/34381
;  PRIOR FILING DATE: 2003-10-28
;  PRIOR APPLICATION NUMBER: US 60/422,472
;  PRIOR FILING DATE: 2002-10-29
;  NUMBER OF SEQ ID NOS: 2442
; SEQ ID NO 141
;   LENGTH: 1220
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-533-069-141

  Query Match             33.8%;  Score 35.5;  DB 1;  Length 1220;
  Best Local Similarity   38.5%;  Pred. No. 1.1e+02;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    5;  Gaps    1;

Qy          1 PVLDLFRE-----LLNELLEALKQKL 21
              |:|  ::|     | :||:  ||| |
Db        946 PLLVAYKEDEIPVLKDELIHELKQTL 971


RESULT 14
US-11-657-313-3
; Sequence 3, Application US/11657313
; Publication No. US20070186295A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Chelsky, Daniel
;  APPLICANT:  Kearney, Paul E.
;  APPLICANT:  Paramithiotis, Eustache
;  APPLICANT:  Hamaidi, Lyes
;  APPLICANT:  Kondejewski, Leslie H.
;  APPLICANT:  Lanoix, Joel
;  APPLICANT:  Hugo, Patrice
;  TITLE OF INVENTION: TAT-036 and Methods of Assessing and Treating Cancer
;  FILE REFERENCE: 50111/090002
;  CURRENT APPLICATION NUMBER: US/11/657,313
;  CURRENT FILING DATE:  2007-01-24
;  PRIOR APPLICATION NUMBER: US 60/762,017
;  PRIOR FILING DATE: 2006-01-25
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
;   LENGTH: 1359
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-657-313-3

  Query Match             33.8%;  Score 35.5;  DB 7;  Length 1359;
  Best Local Similarity   52.4%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    6;  Mismatches    1;  Indels    3;  Gaps    2;

Qy          2 VLDLFRELLNELLEALKQKLK 22
              :|||  :|| |||| |:::|:
Db        435 ILDL--DLLLELLE-LQERLR 452


RESULT 15
US-11-657-313-24
; Sequence 24, Application US/11657313
; Publication No. US20070186295A1
; GENERAL INFORMATION:
;  APPLICANT: Chelsky, Daniel
;  APPLICANT:  Kearney, Paul E.
;  APPLICANT:  Paramithiotis, Eustache
;  APPLICANT:  Hamaidi, Lyes
;  APPLICANT:  Kondejewski, Leslie H.
;  APPLICANT:  Lanoix, Joel
;  APPLICANT:  Hugo, Patrice
;  TITLE OF INVENTION: TAT-036 and Methods of Assessing and Treating Cancer
;  FILE REFERENCE: 50111/090002
;  CURRENT APPLICATION NUMBER: US/11/657,313
;  CURRENT FILING DATE:  2007-01-24
;  PRIOR APPLICATION NUMBER: US 60/762,017
;  PRIOR FILING DATE: 2006-01-25
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
;   LENGTH: 2030
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (896)..(896)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-657-313-24

  Query Match             33.8%;  Score 35.5;  DB 7;  Length 2030;
  Best Local Similarity   52.4%;  Pred. No. 2e+02;
  Matches   11;  Conservative    6;  Mismatches    1;  Indels    3;  Gaps    2;

Qy          2 VLDLFRELLNELLEALKQKLK 22
              :|||  :|| |||| |:::|:
Db       1278 ILDL--DLLLELLE-LQERLR 1295


Search completed: August 16, 2007, 22:55:51
Job time : 7 secs
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: August 16, 2007, 22:39:00 ; Search time 347 Seconds
(without alignments)
67.973 Million cell updates/sec

Title: US-10-715-895A-4
Perfect score: 105
Sequence: 1 PVLDLFRELLNELLEALKQKLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	54.3	1012	2	Q6BNM5_DEBHA	Q6bnm5 debaryomyce
2	55	52.4	892	2	Q3MCF8_ANAVT	Q3mcf8 anabaena va
3	54.5	51.9	216	2	Q65PC9_BACLD	Q65pc9 bacillus li
4	53	50.5	258	2	O09054_RAT	O09054 rattus norv
5	53	50.5	258	2	O08877_RAT	O08877 rattus norv
6	53	50.5	259	1	APOA1_RAT	P04639 rattus norv
7	53	50.5	259	2	Q5EBB2_RAT	Q5ebb2 rattus norv
8	53	50.5	274	1	Y1457_LISMO	P67195 listeria mo
9	53	50.5	274	1	Y1476_LISMF	Q71zl3 listeria mo
10	53	50.5	274	1	Y1494_LISIN	P67196 listeria in
11	53	50.5	274	2	Q4EGJ5_LISMO	Q4egj5 listeria mo
12	53	50.5	274	2	Q4ETW3_LISMO	Q4etw3 listeria mo
13	53	50.5	280	2	Q3K8F1_PSEPF	Q3k8f1 pseudomonas
14	53	50.5	605	2	Q2BAJ7_9BACI	Q2baj7 bacillus sp
15	53	50.5	727	2	Q9FZI5_ARATH	Q9fzi5 arabidopsis
16	53	50.5	876	2	Q9C622_ARATH	Q9c622 arabidopsis
17	52	49.5	224	2	Q5L430_GEOKA	Q5l430 geobacillus
18	52	49.5	969	2	Q5TT78_ANOGA	Q5tt78 anopheles g
19	52	49.5	1125	2	Q23YA8_TETTH	Q23ya8 tetrahymena
20	51	48.6	148	2	Q1VMR9_9FLAO	Q1vmr9 psychroflex
21	51	48.6	366	2	O93601_CHICK	O93601 gallus gall
22	51	48.6	577	1	POF3_SCHPO	O74991 schizosacch
23	50	47.6	277	2	Q885Y6_PSESM	Q885y6 pseudomonas
24	50	47.6	301	2	Q6A254_HAEIN	Q6a254 haemophilus
25	50	47.6	315	2	Q3KPQ9_XENLA	Q3kpq9 xenopus lae
26	50	47.6	317	2	Q4QPB0_HAEI8	Q4qpb0 haemophilus
27	49.5	47.1	261	2	Q25240_LEICH	Q25240 leishmania
28	49.5	47.1	779	2	Q6Z5Z6_ORYSA	Q6z5z6 oryza sativ
29	49	46.7	75	2	Q22N68_TETTH	Q22n68 tetrahymena
30	49	46.7	86	1	Y1679_CLOAB	Q97ig2 clostridium
31	49	46.7	195	1	CA036_HUMAN	Q7z3z2 homo sapien
32	49	46.7	213	2	Q1U9M6_LACRE	Q1u9m6 lactobacill
33	49	46.7	277	2	Q48FH9_PSE14	Q48fh9 pseudomonas
34	49	46.7	277	2	Q4ZQ46_PSEU2	Q4zq46 pseudomonas
35	49	46.7	549	2	Q8SU85_ENCCU	Q8su85 encephalito
36	49	46.7	559	2	Q1VGC0_VIBAL	Q1vgc0 vibrio algi
37	49	46.7	559	2	Q87FD0_VIBPA	Q87fd0 vibrio para
38	49	46.7	569	2	Q1AUZ7_9ACTN	Q1auz7 rubrobacter
39	48.5	46.2	326	2	Q29FC3_DROPS	Q29fc3 drosophila
40	48	45.7	124	2	Q8E5B0_STRA3	Q8e5b0 streptococc
41	48	45.7	228	1	RNC_THETN	Q8r9w3 thermoanaer
42	48	45.7	242	2	Q26IP9_XANP2	Q26ip9 xanthobacte
43	48	45.7	244	2	Q4HJT9_CAMLA	Q4hjt9 campylobact
44	48	45.7	276	2	Q8TN77_METAC	Q8tn77 methanosarc
45	48	45.7	276	2	Q9I523_PSEAE	Q9i523 pseudomonas

ALIGNMENTS

RESULT 1
Q6BNM5_DEBHA
ID Q6BNM5_DEBHA PRELIMINARY; PRT; 1012 AA.
AC Q6BNM5;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Debaryomyces hansenii chromosome E of strain CBS767 of Debaryomyces
DE hansenii.
GN OrderedLocusNames=DEHA0E21714g;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
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CC ---
DR EMBL; CR382137; CAG88468.1; -; Genomic_DNA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR003890; IF_eIF4G.
DR Pfam; PF02854; MIF4G; 2.
DR SMART; SM00543; MIF4G; 1.
KW Complete proteome.
SQ SEQUENCE 1012 AA; 118240 MW; 668882F392B034B8 CRC64;

Query Match 54.3%; Score 57; DB 2; Length 1012;
Best Local Similarity 58.8%; Pred. No. 1.2e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```
Qy          6 FRELLNELLEALKQKLK 22
              :: |:||::| ||||||
Db        522 YKALMNEMIELLKQKLK 538
```

```
RESULT 2
Q3MCF8_ANAVT
ID   Q3MCF8_ANAVT   PRELIMINARY;   PRT;   892 AA.
AC   Q3MCF8;
DT   25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   25-OCT-2005, sequence version 1.
DT   02-MAY-2006, entry version 6.
DE   Hypothetical protein.
GN   OrderedLocusNames=Ava_1706;
OS   Anabaena variabilis (strain ATCC 29413 / PCC 7937).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX   NCBI_TaxID=240292;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Saunders E.H., Schmutz J.,
RA   Larimer F., Land M., Kyrpides N., Mavrommatis K., Richardson P.;
RT   "Complete sequence of Anabaena variabilis ATCC 29413.";
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CP000117; ABA21328.1; -; Genomic_DNA.
DR   GenomeReviews; CP000117_GR; Ava_1706.
DR   InterPro; IPR010989; t-snare.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   892 AA;  104914 MW;  456F1AD7C0451004 CRC64;

  Query Match             52.4%;  Score 55;  DB 2;  Length 892;
  Best Local Similarity   62.5%;  Pred. No. 2e+02;
  Matches   10;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 DLFRELLNELLEALKQ 19
              ||| ||:|||:| ::|
Db        390 DLFNELINELIEKVEQ 405


RESULT 3
Q65PC9_BACLD
ID   Q65PC9_BACLD   PRELIMINARY;   PRT;   216 AA.
AC   Q65PC9; Q62ZR7;
DT   25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   25-OCT-2004, sequence version 1.
DT   27-JUN-2006, entry version 20.
DE   CysE (Serine acetyltransferase).
GN   Name=cysE; OrderedLocusNames=BL03268, BLi00111;
OS   Bacillus licheniformis (strain DSM 13 / ATCC 14580).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=279010;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15383718; DOI=10.1159/000079829;
RA   Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA   Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA   Ehrenreich A., Gottschalk G.;
RT   "The complete genome sequence of Bacillus licheniformis DSM13, an
RT   organism with great industrial potential.";
RL   J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;
RA   Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA   Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,
RA   Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
RA   Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
RA   Ehrlich S.D., Berka R.M.;
RT   "Complete genome sequence of the industrial bacterium Bacillus
RT   licheniformis and comparisons with closely related Bacillus species.";
RL   Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).
CC   -!- CATALYTIC ACTIVITY: Acetyl-CoA + L-serine = CoA + O-acetyl-L-
CC       serine.
CC   -!- PATHWAY: Cysteine biosynthesis.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AE017333; AAU39085.1; -; Genomic_DNA.
DR   EMBL; CP000002; AAU21741.1; -; Genomic_DNA.
DR   GenomeReviews; CP000002_GR; BL03268.
DR   GenomeReviews; AE017333_GR; BLi00111.
DR   GO; GO:0005737; C:cytoplasm; IEA.
DR   GO; GO:0009001; F:serine O-acetyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006535; P:cysteine biosynthesis from serine; IEA.
DR   InterPro; IPR005881; CysE_transferase.
DR   InterPro; IPR001451; Hexapep_transf.
DR   InterPro; IPR011004; Trimer_LpxA_like.
DR   Pfam; PF00132; Hexapep; 4.
DR   TIGRFAMs; TIGR01172; cysE; 1.
KW   Acyltransferase; Amino-acid biosynthesis; Complete proteome;
KW   Cysteine biosynthesis; Repeat; Transferase.
SQ   SEQUENCE   216 AA;  24124 MW;  4C1AD0CC51F74B4C CRC64;

  Query Match             51.9%;  Score 54.5;  DB 2;  Length 216;
  Best Local Similarity   59.1%;  Pred. No. 61;
  Matches   13;  Conservative    4;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              || | |||| ||: : |||:|:
Db        188 PVADRFRELENEIRQ-LKQELR 208


RESULT 4
O09054_RAT
ID   O09054_RAT     PRELIMINARY;   PRT;   258 AA.
AC   O09054;
DT   01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT   01-JUL-1997, sequence version 1.
DT   27-JUN-2006, entry version 25.
DE   Apolipoprotein A-I.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=WKY, and SHRSP; TISSUE=Spleen;
RX   MEDLINE=98077648; PubMed=9415807;
RA   Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RT   "Repetitive elements in the third intron of murine apolipoprotein A-I
RT   gene.";
RL   Biochem. Mol. Biol. Int. 43:989-996(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=WKY, and SHRSP; TISSUE=Spleen;
RA   Chiang A.-N., Fan K.-C., Shaw G.-C., Yang U.-C.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U79578; AAB58430.1; -; Genomic_DNA.
DR   EMBL; U79577; AAB58429.1; -; Genomic_DNA.
DR   HSSP; P02647; 1AV1.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008289; F:lipid binding; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR   InterPro; IPR013326; ApoA/E_ApoLp.
DR   InterPro; IPR000074; ApoA1_A4_E.
DR   Pfam; PF01442; Apolipoprotein; 1.
KW   Lipoprotein.
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SQ   SEQUENCE   258 AA;  29918 MW;  093E6EF2E629CDC8 CRC64;

  Query Match             50.5%;  Score 53;  DB 2;  Length 258;
  Best Local Similarity   54.5%;  Pred. No. 1.1e+02;
  Matches   12;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              | || |:|  || :|| :|||:
Db        121 PHLDEFQEKWNEEVEAYRQKLE 142


RESULT 5
O08877_RAT
ID   O08877_RAT     PRELIMINARY;   PRT;   258 AA.
AC   O08877;
DT   01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT   01-JUL-1997, sequence version 1.
DT   27-JUN-2006, entry version 28.
DE   Apolipoprotein A-I.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=SHR; TISSUE=Spleen;
RX   MEDLINE=98077648; PubMed=9415807;
RA   Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RT   "Repetitive elements in the third intron of murine apolipoprotein A-I
RT   gene.";
RL   Biochem. Mol. Biol. Int. 43:989-996(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=SHR; TISSUE=Spleen;
RA   Chiang A.-N., Fan K.-C., Shaw G.-C., Yang U.-C.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U79576; AAB58428.1; -; Genomic_DNA.
DR   HSSP; P02647; 1AV1.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008289; F:lipid binding; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR   InterPro; IPR013326; ApoA/E_ApoLp.
DR   InterPro; IPR000074; ApoA1_A4_E.
DR   Pfam; PF01442; Apolipoprotein; 1.
KW   Lipoprotein.
SQ   SEQUENCE   258 AA;  29831 MW;  093FB582E629CDC8 CRC64;

  Query Match             50.5%;  Score 53;  DB 2;  Length 258;
  Best Local Similarity   54.5%;  Pred. No. 1.1e+02;
  Matches   12;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              | || |:|  || :|| :|||:
Db        121 PHLDEFQEKWNEEVEAYRQKLE 142


RESULT 6
APOA1_RAT
ID   APOA1_RAT      STANDARD;      PRT;   259 AA.
AC   P04639;
DT   13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT   13-AUG-1987, sequence version 1.
DT   25-JUL-2006, entry version 54.
DE   Apolipoprotein A-I precursor (Apo-AI) (ApoA-I).
GN   Name=Apoa1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84207987; PubMed=6426956;
RA   Poncin J.E., Martial J.A., Gielen J.E.;
RT   "Cloning and structure analysis of the rat apolipoprotein A-I cDNA.";
RL   Eur. J. Biochem. 140:493-498(1984).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87008540; PubMed=3020028;
RA   Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.;
RT   "Linkage, evolution, and expression of the rat apolipoprotein A-I, C-
RT   III, and A-IV genes.";
RL   J. Biol. Chem. 261:13268-13277(1986).
RN   [3]
RP   PROTEIN SEQUENCE OF 1-45.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=82098162; PubMed=6798036;
RA   Gordon J.I., Smith D.P., Andy R., Alpers D.H., Schonfeld G.,
RA   Strauss A.W.;
RT   "The primary translation product of rat intestinal apolipoprotein A-I
RT   mRNA is an unusual preproprotein.";
RL   J. Biol. Chem. 257:971-978(1982).
CC   -!- FUNCTION: Participates in the reverse transport of cholesterol
CC       from tissues to the liver for excretion by promoting cholesterol
CC       efflux from tissues and by acting as a cofactor for the lecithin
CC       cholesterol acyltransferase (LCAT).
CC   -!- SUBCELLULAR LOCATION: Secreted protein.
CC   -!- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC       chylomicrons.
CC   -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; M00001; AAA40749.1; -; mRNA.
DR   EMBL; X00558; CAA25224.1; -; mRNA.
DR   EMBL; J02597; AAA40745.1; -; Genomic_DNA.
DR   PIR; A24700; A24700.
DR   HSSP; P02647; 1AV1.
DR   RGD; 2130; Apoa1.
DR   GO; GO:0017127; F:cholesterol transporter activity; IDA.
DR   GO; GO:0005548; F:phospholipid transporter activity; IDA.
DR   GO; GO:0030301; P:cholesterol transport; IDA.
DR   GO; GO:0015914; P:phospholipid transport; IDA.
DR   InterPro; IPR013326; ApoA/E_ApoLp.
DR   InterPro; IPR000074; ApoA1_A4_E.
DR   Pfam; PF01442; Apolipoprotein; 1.
KW   Cholesterol metabolism; Direct protein sequencing; HDL;
KW   Lipid metabolism; Lipid transport; Repeat; Signal; Steroid metabolism;
KW   Transport.
FT   SIGNAL       1     18
FT   PROPEP      19     24
FT                                /FTId=PRO_0000001953.
FT   CHAIN        25    259       Apolipoprotein A-I.
FT                                /FTId=PRO_0000001954.
FT   REPEAT       67     88       1.
FT   REPEAT       89    110       2.
FT   REPEAT      111    121       3; half-length.
FT   REPEAT      122    143       4.
FT   REPEAT      144    161       5; truncated.
FT   REPEAT      162    183       6.
FT   REPEAT      184    203       7; truncated.
FT   REPEAT      204    225       8.
FT   REPEAT      226    236       9; half-length.
FT   REPEAT      237    259       10.
FT   REGION       67    259       10 X approximate tandem repeats.
FT   CONFLICT    201    201       R -> K (in Ref. 2).
FT   CONFLICT    214    214       G -> S (in Ref. 2).
FT   CONFLICT    218    218       R -> K (in Ref. 2).
SQ   SEQUENCE   259 AA;  30088 MW;  2E8D5EB45FEAEE88 CRC64;
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  Query Match             50.5%;  Score 53;  DB 1;  Length 259;
  Best Local Similarity   54.5%;  Pred. No. 1.1e+02;
  Matches   12;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              | || |:|  || :|| :|||:
Db        122 PHLDEFQEKWNEEVEAYRQKLE 143


RESULT 7
Q5EBB2_RAT
ID   Q5EBB2_RAT     PRELIMINARY;   PRT;   259 AA.
AC   Q5EBB2;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   27-JUN-2006, entry version 6.
DE   Apolipoprotein A-I.
GN   Name=Apoa1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Director MGC Project;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC089820; AAH89820.1; -; mRNA.
DR   UniGene; Rn.10308; -.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008289; F:lipid binding; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   GO; GO:0042157; P:lipoprotein metabolism; IEA.
DR   InterPro; IPR013326; ApoA/E_ApoLp.
DR   InterPro; IPR000074; ApoA1_A4_E.
DR   Pfam; PF01442; Apolipoprotein; 1.
KW   Lipoprotein.
SQ   SEQUENCE   259 AA;  30062 MW;  28538891B2E3A6CD CRC64;

  Query Match             50.5%;  Score 53;  DB 2;  Length 259;
  Best Local Similarity   54.5%;  Pred. No. 1.1e+02;
  Matches   12;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKLK 22
              | || |:|  || :|| :|||:
Db        122 PHLDEFQEKWNEEVEAYRQKLE 143


RESULT 8
Y1457_LISMO
ID   Y1457_LISMO    STANDARD;      PRT;   274 AA.
AC   P67195; Q92BQ3;
DT   11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT   11-OCT-2004, sequence version 1.
DT   30-MAY-2006, entry version 9.
DE   UPF0085 protein lmo1457.
GN   OrderedLocusNames=lmo1457;
OS   Listeria monocytogenes.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1639;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=ATCC BAA-679 / EGD-e / Serovar 1/2a;
RX   MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA   Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA   Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA   Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA   Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA   Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA   Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA   Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA   Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA   Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA   Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA   Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT   "Comparative genomics of Listeria species.";
RL   Science 294:849-852(2001).
CC   -!- SIMILARITY: Belongs to the UPF0085 family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AL591979; CAC99535.1; -; Genomic_DNA.
DR   PIR; AI1256; AI1256.
DR   GenomeReviews; AL591824_GR; lmo1457.
DR   ListiList; LMO01457; -.
DR   LinkHub; P67195; -.
DR   HAMAP; MF_01062; -; 1.
DR   InterPro; IPR005177; DUF299.
DR   Pfam; PF03618; DUF299; 1.
KW   ATP-binding; Complete proteome; Nucleotide-binding.
FT   CHAIN         1    274       UPF0085 protein lmo1457.
FT                                /FTId=PRO_0000196674.
FT   NP_BIND     149    156       ATP (Potential).
SQ   SEQUENCE   274 AA;  30436 MW;  A149AF0F8D5D1B1A CRC64;

  Query Match             50.5%;  Score 53;  DB 1;  Length 274;
  Best Local Similarity   55.0%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQK 20
              |::|||  |||:| |  | |
Db         84 PIIDLFGPLLNQLEETYKIK 103


RESULT 9
Y1476_LISMF
ID   Y1476_LISMF    STANDARD;      PRT;   274 AA.
AC   Q71ZL3;
DT   30-JUL-2004, integrated into UniProtKB/Swiss-Prot.
DT   05-JUL-2004, sequence version 1.
DT   07-MAR-2006, entry version 15.
DE   UPF0085 protein LMOf2365_1476.
GN   OrderedLocusNames=LMOf2365_1476;
OS   Listeria monocytogenes serotype 4b (strain F2365).
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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OX   NCBI_TaxID=265669;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15115801; DOI=10.1093/nar/gkh562;
RA   Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA   Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA   Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA   Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA   Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA   Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,
RA   Bayles D.O., Luchansky J.B., Fraser C.M.;
RT   "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT   borne pathogen Listeria monocytogenes reveal new insights into the
RT   core genome components of this species.";
RL   Nucleic Acids Res. 32:2386-2395(2004).
CC   -!- SIMILARITY: Belongs to the UPF0085 family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE017262; AAT04251.1; -; Genomic_DNA.
DR   GenomeReviews; AE017262_GR; LMOf2365_1476.
DR   TIGR; LMOf2365_1476; -.
DR   HAMAP; MF_01062; -; 1.
DR   InterPro; IPR005177; DUF299.
DR   Pfam; PF03618; DUF299; 1.
KW   ATP-binding; Complete proteome; Nucleotide-binding.
FT   CHAIN         1    274       UPF0085 protein LMOf2365_1476.
FT                                /FTId=PRO_0000196675.
FT   NP_BIND     149    156       ATP (Potential).
SQ   SEQUENCE   274 AA;  30436 MW;  A149AF0F8D5D1B1A CRC64;

  Query Match             50.5%;  Score 53;  DB 1;  Length 274;
  Best Local Similarity   55.0%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQK 20
              |::|||  |||:| |  | |
Db         84 PIIDLFGPLLNQLEETYKIK 103


RESULT 10
Y1494_LISIN
ID   Y1494_LISIN    STANDARD;      PRT;   274 AA.
AC   P67196; Q92BQ3;
DT   11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT   11-OCT-2004, sequence version 1.
DT   07-MAR-2006, entry version 7.
DE   UPF0085 protein lin1494.
GN   OrderedLocusNames=lin1494;
OS   Listeria innocua.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1642;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=CLIP 11262 / Serovar 6a;
RX   MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA   Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA   Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA   Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA   Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA   Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA   Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA   Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA   Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA   Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA   Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA   Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT   "Comparative genomics of Listeria species.";
RL   Science 294:849-852(2001).
CC   -!- SIMILARITY: Belongs to the UPF0085 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL596168; CAC96725.1; -; Genomic_DNA.
DR   PIR; AE1619; AE1619.
DR   GenomeReviews; AL592022_GR; lin1494.
DR   ListiList; LIN01494; -.
DR   HAMAP; MF_01062; -; 1.
DR   InterPro; IPR005177; DUF299.
DR   Pfam; PF03618; DUF299; 1.
KW   ATP-binding; Complete proteome; Nucleotide-binding.
FT   CHAIN         1    274       UPF0085 protein lin1494.
FT                                /FTId=PRO_0000196672.
FT   NP_BIND     149    156       ATP (Potential).
SQ   SEQUENCE   274 AA;  30436 MW;  A149AF0F8D5D1B1A CRC64;

  Query Match             50.5%;  Score 53;  DB 1;  Length 274;
  Best Local Similarity   55.0%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQK 20
              |::|||  |||:| |  | |
Db         84 PIIDLFGPLLNQLEETYKIK 103


RESULT 11
Q4EGJ5_LISMO
ID   Q4EGJ5_LISMO   PRELIMINARY;   PRT;   274 AA.
AC   Q4EGJ5;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   18-APR-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=LMOh7858_1553;
OS   Listeria monocytogenes str. 4b H7858.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=267410;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=4b H7858;
RX   PubMed=15115801; DOI=10.1093/nar/gkh562;
RA   Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA   Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA   Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA   Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA   Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA   Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,
RA   Bayles D.O., Luchansky J.B., Fraser C.M.;
RT   "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT   borne pathogen Listeria monocytogenes reveal new insights into the
RT   core genome components of this species.";
RL   Nucleic Acids Res. 32:2386-2395(2004).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AADR01000035; EAL08910.1; -; Genomic_DNA.
DR   InterPro; IPR005177; DUF299.
DR   Pfam; PF03618; DUF299; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   274 AA;  30436 MW;  A149AF0F8D5D1B1A CRC64;

  Query Match             50.5%;  Score 53;  DB 2;  Length 274;
  Best Local Similarity   55.0%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQK 20
              |::|||  |||:| |  | |
Db         84 PIIDLFGPLLNQLEETYKIK 103
```

```
RESULT 12
Q4ETW3_LISMO
ID   Q4ETW3_LISMO   PRELIMINARY;   PRT;   274 AA.
AC   Q4ETW3;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   18-APR-2006, entry version 3.
DE   Hypothetical protein.
GN   ORFNames=LMOf6854_1500;
OS   Listeria monocytogenes str. 1/2a F6854.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=267409;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=1/2a F6854;
RX   PubMed=15115801; DOI=10.1093/nar/gkh562;
RA   Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA   Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA   Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA   Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA   Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA   Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,
RA   Bayles D.O., Luchansky J.B., Fraser C.M.;
RT   "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT   borne pathogen Listeria monocytogenes reveal new insights into the
RT   core genome components of this species.";
RL   Nucleic Acids Res. 32:2386-2395(2004).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AADQ01000006; EAL07152.1; -; Genomic_DNA.
DR   InterPro; IPR005177; DUF299.
DR   Pfam; PF03618; DUF299; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   274 AA;  30436 MW;  A149AF0F8D5D1B1A CRC64;

  Query Match             50.5%;  Score 53;  DB 2;  Length 274;
  Best Local Similarity   55.0%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQK 20
              |::|||  |||:| |  | |
Db         84 PIIDLFGPLLNQLEETYKIK 103


RESULT 13
Q3K8F1_PSEPF
ID   Q3K8F1_PSEPF   PRELIMINARY;   PRT;   280 AA.
AC   Q3K8F1;
DT   08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT   08-NOV-2005, sequence version 1.
DT   30-MAY-2006, entry version 8.
DE   MazG.
GN   OrderedLocusNames=Pfl_4216;
OS   Pseudomonas fluorescens (strain Pf0-1).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=205922;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   US DOE Joint Genome Institute;
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Saunders E.H., Schmutz J.,
RA   Larimer F., Land M., Kyripides N., Anderson I., Richardson P.;
RT   "Complete sequence of Pseudomonas fluorescens Pf0-1.";
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CP000094; ABA75953.1; -; Genomic_DNA.
DR   GenomeReviews; CP000094_GR; Pfl_4216.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR012199; MazG.
DR   InterPro; IPR011551; MazG_bac.
DR   InterPro; IPR004518; MazG_cat.
DR   Pfam; PF03819; MazG; 2.
DR   PIRSF; PIRSF002844; NTP_pyrphdr_MazG; 1.
DR   TIGRFAMs; TIGR00444; mazG; 1.
KW   Complete proteome.
SQ   SEQUENCE   280 AA;  32085 MW;  0AA804512A53414D CRC64;

  Query Match             50.5%;  Score 53;  DB 2;  Length 280;
  Best Local Similarity   57.9%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQ 19
              ||||  || |:|:|||: :
Db        179 PVLDKVREELDEVLEAMSE 197


RESULT 14
Q2BAJ7_9BACI
ID   Q2BAJ7_9BACI   PRELIMINARY;   PRT;   605 AA.
AC   Q2BAJ7;
DT   04-APR-2006, integrated into UniProtKB/TrEMBL.
DT   04-APR-2006, sequence version 1.
DT   13-JUN-2006, entry version 3.
DE   Oligoendopeptidase F.
GN   ORFNames=B14911_28130;
OS   Bacillus sp. NRRL B-14911.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=313627;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NRRL B-14911;
RA   Siefert J., Ferriera S., Johnson J., Kravitz S., Halpern A.,
RA   Remington K., Beeson K., Tran B., Rogers Y.-H., Friedman R.,
RA   Venter J.C.;
RL   Submitted (FEB-2006) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AAOX01000006; EAR66951.1; -; Genomic_DNA.
DR   GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis; IEA.
DR   InterPro; IPR001567; Pept_M3A_M3B.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR013647; Peptidase_M3_N.
DR   InterPro; IPR004438; Peptidase_M3B.
DR   Pfam; PF01432; Peptidase_M3; 1.
DR   Pfam; PF08439; Peptidase_M3_N; 1.
DR   TIGRFAMs; TIGR00181; pepF; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   605 AA;  68388 MW;  36DEA70199190077 CRC64;

  Query Match             50.5%;  Score 53;  DB 2;  Length 605;
  Best Local Similarity   57.1%;  Pred. No. 2.5e+02;
  Matches   12;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKL 21
              | |: ||: | ||||  | ||
Db        136 PELEAFRKNLEELLETKKHKL 156


RESULT 15
Q9FZI5_ARATH
ID   Q9FZI5_ARATH   PRELIMINARY;   PRT;   727 AA.
```

```
AC   Q9FZI5;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   18-APR-2006, entry version 22.
DE   Hypothetical protein F1O19.1 (Fragment).
GN   Name=F1O19.1;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA   Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A.,
RA   Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA   Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
RA   Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AC007152; AAF98207.1; -; Genomic_DNA.
DR   HSSP; P06239; 3LCK.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
FT   NON_TER       1       1
SQ   SEQUENCE   727 AA;  81129 MW;  BEF55B9646E0459E CRC64;

  Query Match             50.5%;  Score 53;  DB 2;  Length 727;
  Best Local Similarity   52.4%;  Pred. No. 3e+02;
  Matches   11;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKL 21
              |:|| || :|| | |  |:|:
Db        239 PLLDRFRGVLNNLREMCKRKV 259


Search completed: August 16, 2007, 22:48:32
Job time : 351 secs
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GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: August 16, 2007, 22:38:56 ; Search time 213 Seconds
(without alignments)
50.541 Million cell updates/sec

Title: US-10-715-895A-4
Perfect score: 105
Sequence: 1 PVLDLFRELLNELLEALKQKLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	105	100.0	22	2	AAY01708	Aay01708 Peptide f
2	105	100.0	22	2	AAY18683	Aay18683 Lecithin:
3	105	100.0	22	2	AAY18709	Aay18709 Lecithin:
4	105	100.0	22	2	AAY18779	Aay18779 Lecithin:
5	105	100.0	22	2	AAY18963	Aay18963 Lecithin:
6	105	100.0	22	2	AAY18937	Aay18937 Lecithin:
7	105	100.0	22	2	AAY19033	Aay19033 Lecithin:
8	105	100.0	22	2	AAY19191	Aay19191 Lecithin:
9	105	100.0	22	2	AAY19217	Aay19217 Lecithin:
10	105	100.0	22	2	AAY19287	Aay19287 Lecithin:
11	105	100.0	22	2	AAY18446	Aay18446 Lecithin:
12	105	100.0	22	2	AAY18516	Aay18516 Lecithin:
13	105	100.0	22	2	AAY18420	Aay18420 Lecithin:
14	105	100.0	22	8	ADG20900	Adg20900 Apolipopr
15	105	100.0	22	8	ADG20926	Adg20926 Apolipopr
16	105	100.0	22	8	ADG20996	Adg20996 Apolipopr
17	105	100.0	22	8	ADJ32938	Adj32938 Apo lipop
18	105	100.0	22	8	ADJ32886	Adj32886 Apo lipop
19	105	100.0	22	8	ADJ32868	Adj32868 Apo lipop
20	105	100.0	22	8	ADJ32859	Adj32859 Apo lipop
21	105	100.0	22	8	ADJ32842	Adj32842 Apo lipop
22	105	100.0	23	8	ADJ32843	Adj32843 Apo lipop
23	102	97.1	22	2	AAY18686	Aay18686 Lecithin:
24	102	97.1	22	2	AAY18940	Aay18940 Lecithin:
25	102	97.1	22	2	AAY19194	Aay19194 Lecithin:
26	102	97.1	22	2	AAY18423	Aay18423 Lecithin:
27	102	97.1	22	8	ADG20903	Adg20903 Apolipopr
28	102	97.1	22	8	ADJ32845	Adj32845 Apo lipop
29	101	96.2	22	2	AAY18701	Aay18701 Lecithin:
30	101	96.2	22	2	AAY18680	Aay18680 Lecithin:
31	101	96.2	22	2	AAY18934	Aay18934 Lecithin:
32	101	96.2	22	2	AAY18955	Aay18955 Lecithin:
33	101	96.2	22	2	AAY19209	Aay19209 Lecithin:
34	101	96.2	22	2	AAY19188	Aay19188 Lecithin:
35	101	96.2	22	2	AAY18438	Aay18438 Lecithin:
36	101	96.2	22	2	AAY18417	Aay18417 Lecithin:
37	101	96.2	22	8	ADG20918	Adg20918 Apolipopr
38	101	96.2	22	8	ADG20897	Adg20897 Apolipopr
39	101	96.2	22	8	ADJ32839	Adj32839 Apo lipop
40	101	96.2	22	8	ADJ32860	Adj32860 Apo lipop
41	100	95.2	22	2	AAY18685	Aay18685 Lecithin:
42	100	95.2	22	2	AAY18775	Aay18775 Lecithin:
43	100	95.2	22	2	AAY18806	Aay18806 Lecithin:
44	100	95.2	22	2	AAY18705	Aay18705 Lecithin:
45	100	95.2	22	2	AAY18706	Aay18706 Lecithin:

ALIGNMENTS

RESULT 1
AAY01708
ID AAY01708 standard; peptide; 22 AA.
XX
AC AAY01708;
XX
DT 24-JUN-1999 (first entry)
XX
DE Peptide for making peptide-lipid complex by co-lyophilization approach.
XX
KW Peptide-lipid complex; co-lyophilization approach; liposome;
KW compound storage; vaccine; dyslipoproteinemia; hypercholesterolemia;
KW hypertriglyceridemia; low HDL; apolipoprotein A-1 deficiency;
KW cardiovascular disease; atherosclerosis; septic shock;
KW infectious disease.
XX
OS Synthetic.
XX
PN WO9917740-A1.
XX
PD 15-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020330.
XX
PR 02-OCT-1997; 97US-00942597.
XX
PA (DASS/) DASSEUX J.
XX
PI Dasseux J;
XX
DR WPI; 1999-277181/23.
XX
PT Preparation of a lyophilized peptide/lipid product - by co-lyophilization
PT of peptides and solubilizing in lipid.
XX
PS Example 1; Page 18; 42pp; English.
XX
CC The present sequence represents a peptide used to make peptide-lipid
CC complexes by the co-lyophilization approach of the invention. Preparation
CC of a lyophilized peptide/lipid product comprises co-lyophilization of one
CC or more peptides which are able to adopt an amiphipathic conformation or
CC their analogues, and one or more lipids in a solvent system to form a
CC peptide/lipid product which can be rehydrated to form peptide/lipid
CC complexes, solubilizing at least one amphipathic peptide or its analog in
CC a first solution, solubilizing at least one lipid in a second solution

CC which is miscible with the first solution, combining the solutions and
CC lyophilizing to form a product which can be rehydrated to form
CC peptide/lipid complexes. The method is used for for generating stable
CC peptide/lipid vesicles and complexes such as micellar, spherical and
CC discoidal complexes in bulk preparations and in smaller units e.g.
CC dosages. Liposomes are known to be used for delivery vehicles for drugs,
CC cosmetics and bioactive compounds. The method may also be used for
CC storage of compounds which may otherwise be unstable or insoluble in the
CC absence of lipids or for formulation of products for treatment or
CC prevention of human diseases such as co-presentation of antigens in
CC vaccines, treatment or prevention of dyslipoproteinemias, e.g.
CC hypercholesterolemia, hypertriglyceridemia, low HDL and apolipoprotein A-
CC 1 deficiency, cardiovascular disease such as atherosclerosis, septic
CC shock or infectious diseases. The method can also be used in the
CC preparation of complexes which can be used as carriers for drugs, as
CC vectors (to deliver drugs, DNA and genes) e.g. to the liver or to extra
CC hepatic cells or as scavengers to trap toxins such as pesticides and LPS
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 2
AAY18683
ID AAY18683 standard; peptide; 22 AA.
XX
AC AAY18683;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #4.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916408-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020328.
XX
PR 29-SEP-1997; 97US-00940093.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G;
XX
DR WPI; 1999-277031/23.
XX
PT Peptide agonists of apolipoprotein A-I.
XX
PS Example; Page 104; 152pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 14-22 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to
CC AAY18933 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 3
AAY18709
ID AAY18709 standard; peptide; 22 AA.
XX
AC AAY18709;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #30.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916408-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020328.
XX
PR 29-SEP-1997; 97US-00940093.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G;
XX
DR WPI; 1999-277031/23.
XX
PT Peptide agonists of apolipoprotein A-I.
XX
PS Example; Page 105; 152pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 14-22 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at

CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to
CC AAY18933 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 4
AAY18779
ID AAY18779 standard; peptide; 22 AA.
XX
AC AAY18779;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #100.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916408-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020328.
XX
PR 29-SEP-1997; 97US-00940093.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G;
XX
DR WPI; 1999-277031/23.
XX
PT Peptide agonists of apolipoprotein A-I.
XX
PS Example; Page 109; 152pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 14-22 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to
CC AAY18933 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 5
AAY18963
ID AAY18963 standard; peptide; 22 AA.
XX
AC AAY18963;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #30.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916458-A1.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020326.
XX
PR 29-SEP-1997; 97US-00940096.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G;
XX
DR WPI; 1999-277034/23.
XX
PT Peptide agonists of apolipoprotein A-I.
XX
PS Example; Page 108; 254pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
CC AAY19187 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 6
AAY18937
ID AAY18937 standard; peptide; 22 AA.
XX
AC AAY18937;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #4.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916458-A1.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020326.
XX
PR 29-SEP-1997; 97US-00940096.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G;
XX
DR WPI; 1999-277034/23.
XX
PT Peptide agonists of apolipoprotein A-I.
XX
PS Example; Page 107; 254pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
CC AAY19187 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 7
AAY19033
ID AAY19033 standard; peptide; 22 AA.
XX
AC AAY19033;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #100.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916458-A1.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020326.
XX
PR 29-SEP-1997; 97US-00940096.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G;
XX
DR WPI; 1999-277034/23.
XX
PT Peptide agonists of apolipoprotein A-I.
XX
PS Example; Page 112; 254pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
CC AAY19187 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 8
AAY19191
ID AAY19191 standard; peptide; 22 AA.
XX
AC AAY19191;
XX
DT 14-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #4.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;

KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916459-A1.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020327.
XX
PR 29-SEP-1997; 97US-00940095.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX
DR WPI; 1999-277035/23.
XX
PT Peptide agonists of apolipoprotein A-I.
XX
PS Claim 19; Page 155; 280pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY19188 to
CC AAY19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 9
AAY19217
ID AAY19217 standard; peptide; 22 AA.
XX
AC AAY19217;
XX
DT 14-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #30.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916459-A1.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020327.
XX
PR 29-SEP-1997; 97US-00940095.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX
DR WPI; 1999-277035/23.
XX
PT Peptide agonists of apolipoprotein A-I.
XX
PS Example; Page 117; 280pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY19188 to
CC AAY19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 10
AAY19287
ID AAY19287 standard; peptide; 22 AA.
XX
AC AAY19287;
XX
DT 14-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #100.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; human;
KW lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916459-A1.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020327.
XX

PR 29-SEP-1997; 97US-00940095.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX
DR WPI; 1999-277035/23.
XX
PT Peptide agonists of apolipoprotein A-I.
XX
PS Example; Page 121; 280pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I
CC deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY19188 to
CC AAY19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 11
AAY18446
ID AAY18446 standard; peptide; 22 AA.
XX
AC AAY18446;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #30.
XX
KW Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder; ApoA-I;
KW cardiovascular disease; atherosclerosis; restenosis; LCAT;
KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916409-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020329.
XX
PR 29-SEP-1997; 97US-00940136.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX
DR WPI; 1999-254921/21.
XX
PT Nucleic acid encoding apoproteinA-I agonist peptides.
XX
PS Example; Page 135; 232pp; English.
XX
CC The present invention describes a nucleic acid (A) encoding an
CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
CC which forms an amphipathic alpha-helix in presence of lipids. (A),
CC optionally as a complex with lipids, and host cells that contain (A), are
CC useful for gene therapy, or prevention, of diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
CC endotoxemia (septic shock). Host cells containing (A) can also be used to
CC study the role of apoA-I in lipid metabolism. (B) can be used
CC diagnostically, e.g. to measure serum HDL (particularly its subpopulation
CC involved in retrograde cholesterol transport) and for imaging the
CC circulatory system or HDL accumulations at fatty streaks. The present
CC sequence represents a peptide from the present invention
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 12
AAY18516
ID AAY18516 standard; peptide; 22 AA.
XX
AC AAY18516;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #100.
XX
KW Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder; ApoA-I;
KW cardiovascular disease; atherosclerosis; restenosis; LCAT;
KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916409-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020329.
XX
PR 29-SEP-1997; 97US-00940136.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX
DR WPI; 1999-254921/21.
XX
PT Nucleic acid encoding apoproteinA-I agonist peptides.
XX

PS Example; Page 157; 232pp; English.
XX
CC The present invention describes a nucleic acid (A) encoding an
CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
CC which forms an amphipathic alpha-helix in presence of lipids. (A),
CC optionally as a complex with lipids, and host cells that contain (A), are
CC useful for gene therapy, or prevention, of diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
CC endotoxemia (septic shock). Host cells containing (A) can also be used to
CC study the role of apoA-I in lipid metabolism. (B) can be used
CC diagnostically, e.g. to measure serum HDL (particularly its subpopulation
CC involved in retrograde cholesterol transport) and for imaging the
CC circulatory system or HDL accumulations at fatty streaks. The present
CC sequence represents a peptide from the present invention
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 13
AAY18420
ID AAY18420 standard; peptide; 22 AA.
XX
AC AAY18420;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #4.
XX
KW Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder; ApoA-I;
KW cardiovascular disease; atherosclerosis; restenosis; LCAT;
KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916409-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US020329.
XX
PR 29-SEP-1997; 97US-00940136.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX
DR WPI; 1999-254921/21.
XX
PT Nucleic acid encoding apoproteinA-I agonist peptides.
XX
PS Claim 18; Page 127; 232pp; English.
XX
CC The present invention describes a nucleic acid (A) encoding an
CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
CC which forms an amphipathic alpha-helix in presence of lipids. (A),
CC optionally as a complex with lipids, and host cells that contain (A), are
CC useful for gene therapy, or prevention, of diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
CC endotoxemia (septic shock). Host cells containing (A) can also be used to
CC study the role of apoA-I in lipid metabolism. (B) can be used
CC diagnostically, e.g. to measure serum HDL (particularly its subpopulation
CC involved in retrograde cholesterol transport) and for imaging the
CC circulatory system or HDL accumulations at fatty streaks. The present
CC sequence represents a peptide from the present invention
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
||||||||||||||||||||||
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 14
ADG20900
ID ADG20900 standard; peptide; 22 AA.
XX
AC ADG20900;
XX
DT 26-FEB-2004 (first entry)
XX
DE Apolipoprotein A-I agonist peptide seq id 4.
XX
KW apolipoprotein A-I; ApoA-I; agonist; peptide analogue;
KW amphipathic alpha-helix; dyslipidaemia; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis;
KW high density lipoprotein; HDL; Apia-I deficiency; hypertriglyceridaemia;
KW metabolic syndrome; septic shock.
XX
OS Synthetic.
XX
PN US2003203842-A1.
XX
PD 30-OCT-2003.
XX
PF 15-MAR-2002; 2002US-00099836.
XX
PR 01-DEC-1999; 99US-00453834.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX
DR WPI; 2004-010524/01.
XX
PT Novel apolipoprotein agonist treating subject suffering from disorder
PT associated with dyslipidemia such as hypercholesterolemia, cardiovascular
PT disease, atherosclerosis, restenosis, hypertriglyceridemia or metabolic
PT syndrome.
XX
PS Claim 19; SEQ ID NO 4; 146pp; English.
XX
CC The invention describes an apolipoprotein A-I (ApoA-I) agonist (A)
CC comprising a 15-29 residue peptide or peptide analogue which forms an
CC amphipathic alpha-helix in the presence of lipids or its salt. (A) is
CC useful for treating a subject suffering from a disorder associated with
CC dyslipidaemia (hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, high density lipoprotein (HDL) or Apia-I
CC deficiency, hypertriglyceridaemia or metabolic syndrome) or septic shock.
CC This is the amino acid sequence of a ApoA-I agonist peptide.

XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22
Db 1 PVLDLFRELLNELLEALKQKLK 22

RESULT 15
ADG20926
ID ADG20926 standard; peptide; 22 AA.
XX
AC ADG20926;
XX
DT 26-FEB-2004 (first entry)
XX
DE Apolipoprotein A-I agonist peptide seq id 30.
XX
KW apolipoprotein A-I; ApoA-I; agonist; peptide analogue;
KW amphipathic alpha-helix; dyslipidaemia; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis;
KW high density lipoprotein; HDL; Apia-I deficiency; hypertriglyceridaemia;
KW metabolic syndrome; septic shock.
XX
OS Synthetic.
XX
PN US2003203842-A1.
XX
PD 30-OCT-2003.
XX
PF 15-MAR-2002; 2002US-00099836.
XX
PR 01-DEC-1999; 99US-00453834.
XX
PA (DASS/) DASSEUX J.
PA (SEKU/) SEKUL R.
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (METZ/) METZ G.
PA (DUFO/) DUFOURCQ J.
XX
PI Dasseux J, Sekul R, Buttner K, Cornut I, Metz G, Dufourcq J;
XX
DR WPI; 2004-010524/01.
XX
PT Novel apolipoprotein agonist treating subject suffering from disorder
PT associated with dyslipidemia such as hypercholesterolemia, cardiovascular
PT disease, atherosclerosis, restenosis, hypertriglyceridemia or metabolic
PT syndrome.
XX
PS Claim 19; SEQ ID NO 30; 146pp; English.
XX
CC The invention describes an apolipoprotein A-I (ApoA-I) agonist (A)
CC comprising a 15-29 residue peptide or peptide analogue which forms an
CC amphipathic alpha-helix in the presence of lipids or its salt. (A) is
CC useful for treating a subject suffering from a disorder associated with
CC dyslipidaemia (hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, high density lipoprotein (HDL) or Apia-I
CC deficiency, hypertriglyceridaemia or metabolic syndrome) or septic shock.
CC This is the amino acid sequence of a ApoA-I agonist peptide.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 105; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLFRELLNELLEALKQKLK 22

Db 1 PVLDLFRELLNELLEALKQKLK 22

Search completed: August 16, 2007, 22:42:37
Job time : 214 secs

GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: August 16, 2007, 22:42:55 ; Search time 39 Seconds
(without alignments)
54.276 Million cell updates/sec

Title: US-10-715-895A-4
Perfect score: 105
Sequence: 1 PVLDLFRELLNELLEALKQKLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	50.5	259	2	A24700	apolipoprotein A-I
2	53	50.5	274	2	AI1256	hypothetical prote
3	53	50.5	274	2	AE1619	hypothetical prote
4	53	50.5	876	2	B96693	probable receptor
5	52	49.5	225	1	E53402	serine O-acetyltra
6	51	48.6	577	2	T41727	F-box domain prote
7	49	46.7	86	2	B97107	hypothetical prote
8	49	46.7	195	2	JC8002	C1orf36 protein -
9	48	45.7	276	2	G83527	conserved hypothet
10	48	45.7	325	2	F70440	conserved hypothet
11	47	44.8	303	2	H81395	probable ferrochel
12	47	44.8	344	2	C69453	transposase homolo
13	47	44.8	478	2	JC5670	lysosomal membrane
14	47	44.8	738	2	A53542	brefeldin A-sensit
15	47	44.8	1082	1	RNEGB	DNA-directed RNA p
16	46	43.8	179	2	G70325	transcription regu
17	46	43.8	242	2	D97229	probable pseudouri
18	46	43.8	291	2	C71877	hypothetical prote
19	46	43.8	317	2	G59103	hypothetical prote
20	46	43.8	379	2	AD1446	Protein gp4 (Bacte
21	46	43.8	414	2	E64387	hypothetical prote
22	46	43.8	438	2	AB1140	6-phospho-beta-glu
23	46	43.8	548	2	G97047	single-stranded-DN
24	46	43.8	566	2	E81404	acetolactate synth
25	45.5	43.3	327	2	E71130	probable oligopept
26	45	42.9	199	2	E96926	uracyl DNA glycosi
27	45	42.9	335	2	C83927	transcription regu
28	45	42.9	379	2	AB1362	Protein gp4 [Bacte
29	45	42.9	558	2	D81689	conserved hypothet
30	45	42.9	1926	2	S01169	beta-glycosidase c
31	45	42.9	1927	2	S01168	beta-glycosidase c
32	44.5	42.4	229	2	F83663	serine O-acetyltra
33	44	41.9	147	2	D81404	hypothetical prote
34	44	41.9	258	2	T35147	glutamate uptake s
35	44	41.9	438	2	AF1498	6-phospho-beta-glu
36	44	41.9	446	2	T41091	conserved hypothet
37	44	41.9	499	2	S47160	DNA-directed RNA p
38	44	41.9	590	2	H81797	DNA primase (EC 2.
39	44	41.9	631	1	A48346	cell fusion glycop
40	44	41.9	631	1	VGNZPD	cell fusion glycop
41	44	41.9	790	2	E89851	ribonuclease R [im
42	44	41.9	857	2	E84600	probable kinesin h
43	44	41.9	909	2	H86350	hypothetical prote
44	44	41.9	950	2	E70203	exonuclease SbcC (
45	44	41.9	1071	2	F39845	carbamoyl-phosphat

ALIGNMENTS

RESULT 1
A24700
apolipoprotein A-I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24700; S00298; A05314
R;Haddad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J. Biol. Chem. 261, 13268-13277, 1986
A;Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A-I
A;Reference number: A92558; MUID:87008540; PMID:3020028
A;Accession: A24700
A;Molecule type: DNA
A;Residues: 1-259 <HAD>
A;Cross-references: UNIPROT:P04639; UNIPARC:UPI0000168276; EMBL:J02597; NID:g202935; PIDN
R;Poncin, J.E.; Martial, J.A.; Gielen, J.E.
Eur. J. Biochem. 140, 493-498, 1984
A;Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.
A;Reference number: S00298; MUID:84207987; PMID:6426956
A;Accession: S00298
A;Molecule type: mRNA
A;Residues: 1-259 <PON>
A;Cross-references: UNIPARC:UPI0000168276; GB:M00001; EMBL:X00558; NID:g202944; PIDN:AAA
R;Gordon, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Strauss, A.W.
J. Biol. Chem. 257, 971-978, 1982
A;Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is an
A;Reference number: A05314; MUID:82098162; PMID:6798036
A;Accession: A05314
A;Molecule type: protein
A;Residues: 1-18,'X',20-21,'X',23-28,'X',30-38,'X',40-41,'X',43-45 <GOR>
A;Cross-references: UNIPARC:UPI0000177798
C;Comment: This protein is synthesized in the liver and small intestine. The propeptide i
C;Comment: This protein is a major component of the high density lipoproteins in plasma.
C;Genetics:
A;Introns: 15/1; 66/2
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipo
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-259/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 50.5%; Score 53; DB 2; Length 259;
Best Local Similarity 54.5%; Pred. No. 8.3;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 PVLDLFRELLNELLEALKQKLK 22
              | || |:|  || :|| :|||:
Db        122 PHLDEFQEKWNEEVEAYRQKLE 143
```

RESULT 2
AI1256
hypothetical protein lmo1457 [imported] - Listeria monocytogenes (strain EGD-e)

```
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AI1256
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AI1256
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <GLA>
A;Cross-references: UNIPROT:Q92BQ3; UNIPARC:UPI00000553A4; GB:NC_003210; PIDN:CAC99535.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1457
C;Superfamily: ydiA protein

  Query Match             50.5%;  Score 53;  DB 2;  Length 274;
  Best Local Similarity   55.0%;  Pred. No. 8.8;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQK 20
              |::|||  |||:| |  | |
Db         84 PIIDLFGPLLNQLEETYKIK 103


RESULT 3
AE1619
hypothetical protein homolog lin1494 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1619
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <GLA>
A;Cross-references: UNIPROT:Q92BQ3; UNIPARC:UPI00000553A4; GB:AL592022; PIDN:CAC96725.1;
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1494
C;Superfamily: ydiA protein

  Query Match             50.5%;  Score 53;  DB 2;  Length 274;
  Best Local Similarity   55.0%;  Pred. No. 8.8;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQK 20
              |::|||  |||:| |  | |
Db         84 PIIDLFGPLLNQLEETYKIK 103


RESULT 4
B96693
probable receptor serine/threonine kinase PR5K T4O24.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B96693
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96693
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-876 <STO>
A;Cross-references: UNIPROT:Q9C622; UNIPARC:UPI000004840F; GB:AE005173; NID:g11128393; PI
C;Genetics:
A;Gene: T4O24.2
A;Map position: 1

  Query Match             50.5%;  Score 53;  DB 2;  Length 876;
  Best Local Similarity   52.4%;  Pred. No. 29;
  Matches   11;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKL 21
              |:|| || :|| | |  |:|:
Db        388 PLLDRFRGVLNNLREMCKRKV 408


RESULT 5
E53402
serine O-acetyltransferase (EC 2.3.1.30) cysE [similarity] - Bacillus stearothermophilus
C;Species: Bacillus stearothermophilus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C;Accession: E53402
R;Gagnon, Y.; Breton, R.; Putzer, H.; Pelchat, M.; Grunberg-Manago, M.; Lapointe, J.
J. Biol. Chem. 269, 7473-7482, 1994
A;Title: Clustering and co-transcription of the Bacillus subtilis genes encoding the amir

A;Reference number: A53402; MUID:94171772; PMID:7510287
A;Accession: E53402
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-225 <GAG>
A;Cross-references: UNIPARC:UPI0000172390
C;Genetics:
A;Gene: cysE
C;Function:
A;Pathway: cysteine biosynthesis
A;Note: rate-limiting step
C;Superfamily: Bacillus serine acetyltransferase; serine acetyltransferase homology
C;Keywords: acyltransferase; coenzyme A
F;9-169/Domain: serine acetyltransferase homology <SAT>

  Query Match             49.5%;  Score 52;  DB 1;  Length 225;
  Best Local Similarity   50.0%;  Pred. No. 9.8;
  Matches   13;  Conservative    3;  Mismatches    4;  Indels    6;  Gaps    1;

Qy          1 PVLDLFRELLNEL------LEALKQK 20
              |: | ||||  |:      ||||||:
Db        188 PIADRFRELEEEIVRLKSELEALKQQ 213


RESULT 6
T41727
F-box domain protein Pof3p - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41727
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z22013
A;Accession: T41727
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-577 <LYN>
A;Cross-references: UNIPROT:O74991; UNIPARC:UPI0000131DBC; EMBL:AL023781; PIDN:CAA19347.1
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A;Experimental source: strain 972h-; cosmid c338
C;Genetics:
A;Gene: pof3; SPDB:SPCC338.16
A;Map position: 3

  Query Match           48.6%;  Score 51;  DB 2;  Length 577;
  Best Local Similarity  57.1%;  Pred. No. 35;
  Matches   12;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQKL 21
              ||||||| |  |:|  : |:|
Db        131 PVLDLFRILPREVLLCILQQL 151


RESULT 7
B97107
hypothetical protein CAC1679 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97107
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97107
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <KUR>
A;Cross-references: UNIPROT:Q97IG2; UNIPARC:UPI00000CA2A9; GB:AE001437; PIDN:AAK79645.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1679

  Query Match           46.7%;  Score 49;  DB 2;  Length 86;
  Best Local Similarity  52.9%;  Pred. No. 9.2;
  Matches    9;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 DLFRELLNELLEALKQK 20
              || :|:|||:  :||:|
Db         20 DLTKEILNEVYNSLKEK 36


RESULT 8
JC8002
C1orf36 protein - human
C;Species: Homo sapiens (man)
C;Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003
C;Accession: JC8002
R;Lavorgna, G.; Lestingi, M.; Ziviello, C.; Testa, F.; Simonelli, F.; Manitto, M.P.; Bra
Biochem. Biophys. Res. Commun. 308, 414-421, 2003
A;Title: Identification and characterization of C1orf36, a transcript highly expressed i
A;Reference number: JC8002; PMID:12914764
A;Accession: JC8002
A;Molecule type: mRNA
A;Residues: 1-195 <LAV>
A;Cross-references: GB:AY191519
C;Comment: This protein is a evolutionary conserved phosphorylated protein that has a mi
C;Genetics:
A;Gene: c1orf36
A;Map position: chromosme 1q32.3
C;Keywords: C1orf36; coiled-coil; mitochondrial function

  Query Match           46.7%;  Score 49;  DB 2;  Length 195;
  Best Local Similarity  52.6%;  Pred. No. 21;
  Matches   10;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 VLDLFRELLNELLEALKQK 20
              |  ||| :| |:|| :||:
Db        114 VSQLFRSVLQEVLERMKQE 132


RESULT 9
G83527
conserved hypothetical protein PA0935 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83527
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83527
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <STO>
A;Cross-references: UNIPROT:Q9I523; UNIPARC:UPI00000C51C7; GB:AE004528; GB:AE004091; NID:
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0935
C;Superfamily: nucleoside triphosphate pyrophosphohydrolase MazG; beta-lactamase regulato

  Query Match           45.7%;  Score 48;  DB 2;  Length 276;
  Best Local Similarity  52.6%;  Pred. No. 42;
  Matches   10;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 PVLDLFRELLNELLEALKQ 19
              ||:|  || |:|:|||: :
Db        176 PVVDKVREGLDEVLEAMAE 194


RESULT 10
F70440
conserved hypothetical protein aq_1630 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70440
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70440
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-325 <AQF>
A;Cross-references: UNIPROT:O67552; UNIPARC:UPI0000056687; GB:AE000748; NID:g2983960; PID
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1630
C;Superfamily: Mycoplasma conserved hypothetical protein MG190

  Query Match           45.7%;  Score 48;  DB 2;  Length 325;
  Best Local Similarity  52.9%;  Pred. No. 49;
  Matches    9;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 FRELLNELLEALKQKLK 22
              : | | :||||:|::||
Db        303 YEEALKKLLEAIKEELK 319


RESULT 11
H81395
probable ferrochelatase (EC 4.99.1.1) Cj0503c [imported] - Campylobacter jejuni (strain N
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81395
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: H81395
A;Status: preliminary
```

A;Molecule type: DNA
A;Residues: 1-303 <PAR>
A;Cross-references: UNIPROT:Q9PI08; UNIPARC:UPI000012C5CC; GB:AL139075; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0501; Cj0503c
C;Keywords: lyase

Query Match 44.8%; Score 47; DB 2; Length 303;
Best Local Similarity 47.4%; Pred. No. 62;
Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 4 DLFRELLNELLEALKQKLK 22
||: : :|: :| ||:|||
Db 196 DLYEKHVNDHVEILKEKLK 214

RESULT 12
C69453
transposase homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69453
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69453
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-344 <KLE>
A;Cross-references: UNIPROT:O28645; UNIPARC:UPI0000056C62; GB:AE000990; GB:AE000782; NID

Query Match 44.8%; Score 47; DB 2; Length 344;
Best Local Similarity 52.9%; Pred. No. 71;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 6 FRELLNELLEALKQKLK 22
:|:|: :| | ||| ||
Db 267 YRKLVRKLFEGLKQNLK 283

RESULT 13
JC5670
lysosomal membrane 85K glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004
C;Accession: JC5670
R;Tabuchi, N.; Akasaki, K.; Sasaki, T.; Kanda, N.; Tsuji, H.
J. Biochem. 122, 756-763, 1997
A;Title: Identification and characterization of a major lysosomal membrane glycoprotein,
A;Reference number: JC5670; MUID:98060500; PMID:9399579
A;Accession: JC5670
A;Molecule type: mRNA
A;Residues: 1-478 <TAB>
A;Cross-references: UNIPROT:O35114; UNIPARC:UPI00000231D6; GB:AB008553; NID:g2618485; PI
C;Comment: This protein is involved in sequestration of particular cytoplasmic proteins
C;Superfamily: lysosomal integral membrane protein II
F;1-26/Domain: signal sequence #status predicted <SIG>
F;433-458/Domain: transmembrane #status predicted <TMM>
F;474-475/Region: endosomal/lysosomal sorting signal

Query Match 44.8%; Score 47; DB 2; Length 478;
Best Local Similarity 52.6%; Pred. No. 1e+02;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 LDLFRELLNELLEALKQKL 21
| | |||: :|:| :|||
Db 149 LTLLRELIEAMLKAYQQKL 167

RESULT 14
A53542
brefeldin A-sensitive Golgi protein LDLC - human
C;Species: Homo sapiens (man)
C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 09-Jul-2004
C;Accession: A53542
R;Podos, S.D.; Reddy, P.; Ashkenas, J.; Krieger, M.
J. Cell Biol. 127, 679-691, 1994
A;Title: LDLC encodes a brefeldin A-sensitive, peripheral Golgi protein required for norm
A;Reference number: A53542; MUID:95050941; PMID:7962052
A;Accession: A53542
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-738 <POD>
A;Cross-references: UNIPROT:Q14746; UNIPARC:UPI0000127E38; GB:Z34975; NID:g575653; PIDN:C
C;Genetics:
A;Gene: LDLC
C;Keywords: Golgi apparatus

Query Match 44.8%; Score 47; DB 2; Length 738;
Best Local Similarity 55.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 LDLFRELLNELLEALKQKLK 22
|| :| | |||| :| ||:
Db 520 LDKLQEQLPELLEIIKPKLE 539

RESULT 15
RNEGB
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Euglena gracilis chloroplast
C;Species: chloroplast Euglena gracilis
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S09210
R;Yepiz-Plascencia, G.M.; Radebaugh, C.A.; Hallick, R.B.
Nucleic Acids Res. 18, 1869-1878, 1990
A;Title: The Euglena gracilis chloroplast rpoB gene. Novel gene organization and transcri
A;Reference number: S09210; MUID:90245579; PMID:2110656
A;Accession: S09210
A;Molecule type: DNA
A;Residues: 1-1082 <YEP>
A;Cross-references: UNIPROT:P23579; UNIPARC:UPI00001346D7; EMBL:X17191; NID:g11501; PIDN:
A;Note: the authors translated the codon CGT for residue 132 as Gly
C;Genetics:
A;Gene: rpoB
A;Genome: chloroplast
A;Introns: 13/3; 89/2; 117/1; 154/3; 227/3; 241/1; 288/2; 732/3
C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 44.8%; Score 47; DB 1; Length 1082;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FRELLNELLEALKQKL 21
|| :|||| :||:||
Db 314 FRIILNELESSLKEKL 329

Search completed: August 16, 2007, 22:49:16
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Thursday, August 16, 2007

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From: HUYEN-TRAN TON-NU
Location: EIC 1600
REM-1D58 / REM-1B61
Phone: (571)272-9218

huyen-tran.ton-nu@uspto.gov

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